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US-09-531-914-4
US-09-531-914-5
US-09-531-914-9
US-09-908-988B-4
US-09-949-016-8267
US-09-949-016-8267
US-08-973-462-8
US-09-329-418-8
US-09-329-418-8
US-09-329-418-8
US-09-17-5328-6287
US-08-736-770-6
US-08-736-770-6
US-09-702-705-1809
US-09-702-705-1809
US-09-643-657-4
US-09-643-657-4
US-09-643-657-4
US-09-643-657-4
US-09-49-016-7735

Sequence 4, Appli Sequence 9, Appli Sequence 9, Appli Sequence 10660, A Sequence 8267, Appli Sequence 8, Appli Sequence 8, Appli Sequence 6287, Ap Sequence 6287, Ap Sequence 1809, Ap

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Minimum DB
Maximum DB
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Maximum Match :0(*
Listing first 45 summaries
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Perfect score:
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seq length: 20000000000
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1: /cgn2_6/ptoc.it a/1/iaa/5A_COMB.pep:*

2: /cgn2_6/ptoc.it a/1/iaa/5B_COMB.pep:*

3: /cgn2_6/ptoc.it a/1/iaa/6A_COMB.pep:*

4: /cgn2_6/ptoc.it a/1/iaa/B_COMB.pep:*

5: /cgn2_6/ptoc.it a/1/iaa/PCTUS_COMB.pep:*

5: /cgn2_6/ptoc.it a/1/iaa/backfiles1.pep:*
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Gapop 10.0 , Garext 0.
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   Gei.Core version 5.1.6 (c) 1993 - 2005 Compugen Ltd
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3 US-09-189-527-7

3 US-09-189-527-4

4 US-09-48-116-10835

4 US-09-585-1738-12

3 US-08-922-635-22

4 US-08-922-635-5

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4 US-09-389-487-6

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4 US-09-588-1738-51

4 US-09-588-1738-51

4 US-09-588-1738-51

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Sequence 13, Appl
Sequence 4, Appli
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Sequence 10835, A
Sequence 22, Appli
Sequence 22, Appli
Sequence 5, Appli
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Sequence 7561, Appli
Sequence 7561, Appli
Sequence 2, Appli
Sequence 25, Appli
Sequence 26, Appli
Sequence 27, Appli
Sequence 28, Appli
Sequence 29, Appli
Sequence 19048, A
Sequence 94, Appli
Sequence 94, Appli
Sequence 94, Appli
Sequence 3947, A
Sequence 3947, A
Sequence 3, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 9, Appli
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## Best Available Copy

RESULT 2 US-09-189-527-7 ; Sequence 7, Application US/09189527A ; Patent No. 6387639

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"CURRENT APPLICATION NUMBER: US/09/189,527A
CURRENT FILING DATE: 1998-11-10
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FRSTSEQ for Windows Version 3.0
SEQ ID NO 4
LENGTH: 329
TYPE: PRT
ORGANISM: homo sapiens
US-09-189-527-4
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APPLICANT: Myrna R. Rosenfeld
TITLE OF INVENTION: Ma Family Polypeptides and
TITLE OF INVENTION: Antibodies
FILE REFERENCE: SIK98-01
CURRENT APPLICATION NUMBER: US/09/189,527A
CURRENT FILING DATE: 1998-11-10
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 7
SEQ ID NO 7
TYPE: PRT
ORGANISM: homo sapiens
US-09-189-527-7
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Patent No. 6387639
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 38.6%; Score 564; DB 3; Length 329; Best Local Similarity 47.0%; Pred. No. 8.7e-51; Antiches 117; Conservative 47; Mismatches 73; Indels
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40.6%; Score 593; DB 3; Length 195;
Best Local Similarity 98.3%; Pred. No. 3.5e-54;
Matches 113; Conservative 1; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Jerome B. Posner ...'
APPLICANT: Josep C. Dalmau ,
APPLICANT: Myrna R. Rosenfeld
TITLE OF INVENTION: Ma Family Polypeptides and Anti-Ma
TITLE OF INVENTION: Antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE:
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                                                               259
                                                                                                          182
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                                                                                                                                                                                               122 KRWLAESLRGPALDLMHIVQADNPSISVEECLEAFKQVFGSLESRRTAQVRYLKTYQEEG 181
                                                                                                                                                                                                                                               139 EMLNYILDNVIQPLVESIWYKRLTLFSGKGHPRAWRGNFDPWLEHTNEVLEEWQVSDVEK 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         141 LAHLLGQAMAHAPQPLLPMRYRKLRVFSGSAVPAPEEESFEVWLEQATEIVKEWP 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 LAHLLGQAMAHAPQPLLPMRYRKLRVFSGSAVPAPEEESFEVWLEQATEIVKEWP 115
                                                                                                                                                                                                                                                                                          63 HLLGQAMAHAPQPLL-PMRYRKLRVFSGSAVPAPEEESFEVWLEQATEIVKEWPVTEAEK 121
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                                                                                     EKVSAYVLRLETLLRKAVELRAIPRRIADQVRLEQVMAGA----TLNQMLMCRLRELKDQ 237
                                                                                                                                                       RRRLMESIRGPAADVIRILESUNPAITTAECLKALEQVEGSVESSRDAQIKFLUTYQNPG 258
GPPPSFLEL 246
                                                               EKLSAYVIRLEPLLQKVVEKGAIDKDNVNQARLEQVIAGANHSGAIRRQLWL---TGAGE 315
                                                                                                                                                                                                                                                                                                                                         GKGGVWKVLFKPPTSDAEFLERLHLFLAREGWTVQDVARVLGFQNPTPTP----GPEMPA 138
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                                                                                                                                                                                                                                                                                                                                                                                                                              73; Indels 12;
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PRIOR PILLING DATE: 2000-10-20
PRIOR PELLING DATE: 2000-10-20
PRIOR PELLING DATE: 2000-10-03
PRIOR FILLING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10835
LENGTH: 577
                                                               APPLICANT: Butler, Karlene
APPLICANT: Famodu, Omolayo O.
APPLICANT: Famodu, Cmolayo O.
APPLICANT: Matteridge, Steven
APPLICANT: Maxwell, Carl
APPLICANT: Maxwell, Carl
TITLE OF INVENTION: Magnesium Chelatase
FILE REFERENCE: BB1370 US NA
CURRENT APPLICATION NUMBER: US/09/585,173B
CURRENT APPLICATION NUMBER: US 60/137,461
PRIOR APPLICATION NUMBER: US 60/137,461
PRIOR APPLICATION UNMER: US 60/137,461
PRIOR FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 54
SOFTWARE: Microsoft Office 97
SEQ ID NO 12
LENGTH: 750
                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 5
US-09-585-173B-12
; Sequence 12, Application US/09585173B
; Patent No. 6570063
; GENERAL INFORMATION:
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US-09-585-173B-12
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CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION.
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                          TYPE: PRT
ORGANISM: Glycine max
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           350 YSIIYGRFDSKR-------REGKQLSLHELTINEAAAQFCMRDNTLLLRRVELFSL 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             156 FKQVFGSLESRRTAQVRYLKTYQEEGEKVS-----AYVLRLETLLRKAVEKRAI 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96 EEESFEVWLEQATEIVKEWPVTEAEKKRWLAESLRGPALDLMHIVQADNPSISVEBCLEA 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EPEMVRMVVESVERIFRSFPRGDAGEVTSLLKLNKKLARSVGHIFEMDDNDSQKEEEIRK 349
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6.8%;

Score 100;

DB 4;

Length 750;

24

7.

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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
; LENGTH: 1070
; TYDE: PRT
; ORGANISM: Homo Bapiens
US-08-922-635-22
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Matches
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Best Local Similarity
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EARLIER FILING DATE: 1996-05-20
EARLIER APPLICATION NUMBER: 60,012,600
EARLIER FILING DATE: 1996-03-01
NUMBER OF SEO ID NOS: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Patent No. 6033871
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: DNA MOLECULES ENCODING IMIDALINE RECEPTIVE POLYPEPTIDES TITLE OF INVENTION: AND POLYPEPTIDES ENCODED THEREBY FILE REFERENCE: Corrected Sequence Listing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: PILETZ, John E. APPLICANT: IVANOV, Tina R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           374
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                                                                                                                                        PAGQAASDDLRDVPGAVGGASP----EHAEPEVQVVPGSGQIIFLPFTCIGYTATNQD-
                                                                                                                                                                       PA-----LDLMHIVQADNPSISVEECLEAFKQVF---GSLESRRTAQVRYLKTYQEE 180
                                                                                                                                                                                                          QPIL-----SNQGIMFVQEEALASSLSSTDSLTPEHQPIAQG-----CSDSLESI
                                                                                                                                                                                                                                               QPLLPMRYRKLRVFSGSAVPÅPEEESFEVWLEQATEIVKE-WPVTEAEKKRWLAESLRG- 131
                                                                                                                                                                                                                                                                                  EKELDTVE-VLKAIQKAKEVKSKLSNPEKKGGEDSRLSAAPCIRPSSSPPTVAPASASLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LKDQGPPPSFLELMKVIREEEEEEASFENESIEEPEER 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPVTEAEKKRWLAESLRGPALDLMHIVQADNPSISVEECLEAFKQVFGSLESRRTAQVRY 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GQAMAHAPQPLLPMRYRKLRVFSGSAVPAPEEES--FEVWLEQ-----ATEIVKE
 EQGEE---EDEEEEEEDVÄENRYFEMGPPDVEEEEGGGQGEEEEEE 243

    -QNQPPPPPPPPQNQESGEEQNEEEEQEDDKDEENEQQ 438

                                 PSFLEIMKVIREEEEEEASFENESIE----EPEERDGYGRWNHEGDD 283
                                                                    -----FIQRLSTLIRQAIE, RQLP-------AWIEAANQREEGQG
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                                                                                                                                                                                                                                                                                                                                                                   6.7%; Score 98; 22.6%; Pred. No.
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                                                                                                                                                                                                                                                                                                                                                     ore 98; DB 3; Length 1070; ed. No. 0.54; Mismatches 103; Indels
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                                                                                                                                                                                                                                                                                                                   GOEGVSPATVPCISPELLAHLLGQAMAHAP
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                                                                                                                                                                                                                                                                                                                                                      96;
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CURRENT FILING DATE: 1999-07-30
NUMBER OF SEQ ID NOS: 47
SOFTWARE: PERL Program
SEQ ID NO 2
LENGTH: 1504
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Lal, Preeti
APPLICANT: Tang, Y. Tom
APPLICANT: Baugh, Mariah R.
APPLICANT: Baugh, Mariah R.
APPLICANT: Kaser, Matthew R.
TITLE OF INVENTION: Mammalian Imidazoline Receptor
FILE REFERENCE: PC-0006 US
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Patent No. 647575
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                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY:
OTHER INFORMATION: 129581CD1
PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                        Local
                       241 PSFLELMKVIREEEEEEASFENESIE----EPEERDGYGRWNHEGDD 283
                                                                               602
                                                                                                                       181
                                                                                                                                                             548
634 EQGEE---EDEEEEEEDVAENRYFEMGPPDVEEEEGGGQGEEEEEE
                                                                                                                                                                                                                                          503 QPIL-----SNQGIMFVQEEALASSLSSTDSLTPEHQPIAQG-----CSDSLESI 547
                                                                                                                                                                                                                                                                                                                        444 EKELDTVE-VLKAIQKAKEVKSKLSNPEKKGGEDSRLSAAPCIRPSSSPPTVAPASASLP 502
                                                                                                                                                                                                                                                                              74 QPLLPMRYRKLRVFSGSAVPAPEEESFEVWLEQATEIVKB-WPVTEAEKKRWLAESLRG-
                                                                                                                                                                                                                                                                                                                                                              30 EKEGQTVSGMFRAL-------GQEGVSPATVPCISPELLAHLLGQAMAHAP
                                                                                                                                                                                                                                                                                                                                                                                                        65;
                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                   GEKVSAYVLRLETLLRKAVEKRAIPRRIADQVRLEQVMAGATLNQMLWCRLRELKDQGPP 240
                                                                                                                                                               PAGQAASDDLRDVPGAVGGASP----EHAEPEVQVVPGSGQIIFLPFTCIGYTATNQD-
                                                                               ----FIQRLSTLIRQAIE-RQLP----
                                                                                                                                                                                                   PA-----LDLMHIVQADNPSISVEECLEAFKQVF---GSLESRRTAQVRYLKTYQEE 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Application US/09364206
                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                        103;
                                                                               -----AWIEAANQREEGQG 633
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                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                    131
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US-08-650-766-6

| Sequence 6, Application US/08650766D
| Sequence 6, Application US/08650766D
| Patent No. 6015590
| GENERAL INFORMATION:
| APPLICANT: FILETZ, John E.
| APPLICANT: IVANOV, Tina R.
| TITLE OF INVENTION: DNA SEQUENCE ENCODING A HUMAN IMIDAZOLINE RECEPTOR TITLE OF INVENTION: DNA SEQUENCE ENCODING THE SAME
| TILE OF INVENTION: DNA SEQUENCE ENCODING THE SAME
| TILE OF INVENTION: DNA SEQUENCE ENCODING THE SAME
| TILE OF INVENTION: DNA SEQUENCE ENCODING THE SAME
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| TILE OF INVENTION: DNA SEQUENCE ENCODING THE SAME
| TILE OF INVENTION: DNA SEQUENCE ENCODING THE SAME
| TILE OF INVENTION: NUMBER: US/08/650,766D
| CURRENT APPLICATION NUMBER: US/08/650,766D
| CURRENT FILING DATE: 1996-05-20
| EARLLER FILING DATE: 1996-03-01
| NUMBER OF SEQ ID NOS: 21
| SOFTWARE: PATENTIN Ver. 2.0
| SEQ ID NO 6
| LENGTH: 651
| TYPE: PRT
| ORGANISM: Homo Bapiens
| US-08-650-766-6
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NUMBER OF SEQ ID NOS: 22
; SEQ TWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 651
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-922-635-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match 6.7%; Score 97.5; DB 3; Length 651; Best Local Similarity 23.0%; Pred. No. 0.29; Matches 59; Conservative 30; Mismatches 99; Indels 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/08/922,635A
CURRENT FILING DATE: 1997-09-03
EARLIER APPLICATION NUMBER: 08/650,766
EARLIER FILING DATE: 1996-05-20
JEARLIER APPLICATION NUMBER: 60/012,600
EARLIER FILING DATE: 1996-03-01
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APPLICANT: IVANOV, Tina R.

TITLE OF INVENTION: DNA MOLECULES ENCODING IMIDALINE RECEPTIVE POLYPEPTIDES
TITLE OF INVENTION: AND POLYPEPTIDES ENCODED THEREBY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE: Corrected Sequence Listing
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267 EPEERDGYGRWNHEGDD 283 : || :| |: :: :
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                                                                                                                                                                                                                                                                                                      104 LEQATEIVKE-WPVTEAEKKRWLAESLRG-PA-----LDLMHIVQADNPSISVEECL 153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             211 QVRLEQVMAGATLNOMLWCRLRELKDQGPPPSFLELMKVIREEEBEEASFENESIE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          104 LEQATEIVKE-WPVTEAEKKRWLAESLRG-PA-----LDLMHIVQADNPSISVEECL 153
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                                                                                                                                                                                                                                                                                                                                                                                                   44 GOEGVSPATVPCISPELLAHLLGQAMAHAPOPLLPMRYRKLRVFSGSAVPAPEEESFEVW 103
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                                                                                                                                                                                                          EAFKOVF---GSLESRRTAOVRYLKTYQEEGEKVSAYVLRLETLLRKAVEKRAIPRRIAD 210
                                                                                                                                                                                                                                                                                                                                                      GGEDSRLSAAPCIRPSSSPPTVAPASASLPQPIL------SNQGIMFVQEEALASS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----AWIEAANQREEGOGEOGEE---EDEEEEEEDVAENRYFEMGPP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LSSTDSLTPEHQPIAQG-----CSDSLESIPAGQAASDDLRDVPGAVGGASP-----EHA 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGEDSRLSAAPCIRPS9SPPTVAPASASLPQPIL-----SNQGIMFVQEEALASS 110
                                                                                                             QVRLEQVWAGATLNQMLWCRLRELKDQGPPPSFLELMKVIREEEEEEASFENESIE----
                                                                                                                                                                                                                                                    LSSTDSLTPEHQPIAQG-:---CSDSLESIPAGQAASDDLRDVPGAVGGASP-----EHA
                                                                                                                                                             EPEVQVVPGSGQIIFLPFTCIGYTATNQD-----FIQRLSTLIRQAIE-RQLP----
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                                                                   ------AWIEAANQREEGOGEOGEE---EDEEEEEEDVAENRYFEMGPP 248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     12;
                                                                                                                                                        Sequence 51, Application US/09585173B
Patent No. 6570063
GENERAL INFORMATION:
APPLICANT: Butler, Karlene
APPLICANT: Gutteridge, Steven
APPLICANT: Maxwell, Carl
TITLE OF INVENTION: Magnesium Chelatase
FILE REFERENCE: BB1370 US NA
CURRENT FILING DATE: 2000-06-01
PRIOR APPLICATION NUMBER: US/09/585,173B
CURRENT FILING DATE: 1999-06-04
PRIOR FILING DATE: 1999-06-04
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US-09-585-173B-51
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US-09-389-487-6
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    US-09-585-173B-51
                                                                SOFTWARE: Microsoft Office 97
SEQ ID NO 51
LENGTH: 754
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APPLICANT: PILETZ, John E.

APPLICANT: IVANOV, Tina R.

TITLE OF INVENTION: DAN SEQUENCE ENCODING A HUMAN IMIDAZOLINE RECEPTOR AND TITLE OF INVENTION: METHOD FOR CLONING THE SAME
FILE REFERENCE: Corrected Sequence Listing
Patent No. 6576742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 6, Application US/09389487 Patent No. 6576742
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CURRENT FILING DATE: 1999-09-03
EARLIER APPLICATION NUMBER: US 08/650,766
EARLIER FILING DATE: 1996-05-20
NUMBER OF SEQ ID NOS: 21
                                                                                                                                         NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Homo sapiens
                   TYPE: PRT ORGANISM: Pisum sativum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       249 DVÉEEEGGGQGEEEEEE 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  267 EPEERDGYGRWNHEGDD 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 211 QVRLEQVMAGATLNQMLWCRLRELKDQGPPPSFLELMKVIREEEEEEASFENESIE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             111 LSSTDSLTPEHQPIAQG-----CSDSLESIPAGQAASDDLRDVPGAVGGASP-----EHA 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            104 LEQATEIVKE-WPVTEAEKKRWLÆESLRG-PA-----LDLMHIVQADNPSISVEECL 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      44 GQEGVSPATVPCISPELLAHLLGQAMAHAPQPLLPMRYRKLRVFSGSAVPAPEBESFEVW 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EAFKQVF---GSLESRRTAQVRYLKTYQEEGEKVSAYVLRLETLLRKAVEKRAIPRRIAD 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EPEVQVVPGSGQIIFLPFTCIGYTATNQD-----FIQRLSTLIRQAIE-RQLP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGEDSRLSAAPCIRPSSSPPTVAPASASLPQPIL----SNQGIMFVQEEALASS 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DVEEEEGGGQGEEEEE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---AWIEAANQREEGQGEQGEE---EDEEEEEEDVAENRYFEMGPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 97.5; DB 4;
Pred. No. 0.29;
0; Mismatches 99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99;
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RESULT 12
US-09-949-016-7561
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CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08
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SOFTWARE: FeatSEQ for Windows Version 4.0 SEQ ID NO 7561
LENGTH: 1307
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: WENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 7561, Application US/09949016 Patent No. 6812339
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Best Local Similarity
Matches 60; Conserv
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Human
-09-949-016-7561
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               119 AEKKRWIAESIRGPALDIMHIVQADNPSISVEECLEAFKQVFGSLESRRTAQVRYIKTYQ 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      277
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                                                                                                                                                                                                                                                                                                                                                                                                                          152 CLEAFKOVFGSLESRRTAOVRYLKTYQEEGEKVSAYV------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          845 IKALKEEIGNVQLEKAQQL-----EE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             71 HAPOPILPMRYRKLRVFSGSAVPAPEE------ESFEVWLEQATEIVKEWPVTE 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20 EFLERLNLFLEKEGQTVSGMFRALGQEGVS-----PATVPCISPE---LLAHLLGQAMA 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NLSAD-LPMSFENRVEAVGIATEFODNCGOVFKMVDEDTDNAKTQIILAREYLKDVTISK 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DD------QNQPPPPP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PPPQNQESNEEQNEEEEEQSEEEEDDNDEENEQQ 442
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                                                                                                     QASSFPPHE--ELLKVISEREKEISGLWNELDSLKDAVEHQRKKONERQQQVEAVELEAK 105:
                                                                                                                                              -----SIEEPEERD----
                                                                                                                                                                                                                                   LKEKENELKRIEAMIKERESDISSKTQLLQDVQDE-----NKIFKSQIEQLKQQNYQ 993
                                                                                                                                                                                                                                                                                            -----LRLETLLRKAVEKRAIPRRIADQVRLEQVMAGATLNQMLWCRLRELKDQG-- 238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6.4%; Score 94; DB 4; Length 1307; 18.3%; Pred. No. 1.9; ative 37; Mismatches 70; Indels 1
---GYGRWNH 279
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OF DETECTION AND USES THEREOF
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                                                                                                                                                                             272
                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 14
US-08-556-419-25
; Sequence 25, Applica
; Sequence 10, 6093549
   APPLICANT: Ross, Christopher
APPLICANT: Li, Xiao-Jiang
APPLICANT: Li, Shi-Hua
APPLICANT: Sharp, Alan
APPLICANT: Sharp, Alan
APPLICANT: Worley, Paul
APPLICANT: Worley, Paul
APPLICANT: Myder, Solomon
TITLE OF INVENTION: Huntingtin-associated protein
FILE REFERENCE: 01107.52271
CURRENT APPLICATION NUMBER: US/08/556,419C
CURRENT FILING DATE: 1995-11-09
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSEQ for Windows Version 3.0
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Best Local Similarity
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CURRENT FILING DATE: 1999-03-08
NUMBER OF SEQ ID NOS: 13
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APPLICANT: De Gregorio, Ennio
TITLE OF INVENTION: TRANSLATION DRIVER SYSTEM AND METHODS
FILE REFERENCE: 9882-004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 1560
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     410 SPAQEEEMEEEEE---EEEGEAGEAGEAESEKG----GEELLPPESTPI--PANLSQNL 459
                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            640 TRGPPRGGPGGELPRGPQAGLGPRRSQQGPRKEPRKIIATVLMTEDIKLNKAEKAWKPSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     257 -EASFENESIEEP 268
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14 TPNQDTEFLERLNLFLEKEG------QTVSGMFRALGQEGVSPATVPCISPELLAHLL 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        66 GQAMAHAPQPLLPMRYRKLRVFS------
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22.0%; Pred. No. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -ESRRTAQV-----RYLKTYQEEGEKVSAYVLRLETLLRKAVEKRAIP--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US/09264512B
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LENGTH: 331
TYPE: PRT
ORGANISM: Homo Bapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/660,412
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/603,803
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/201,762
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/201,762
PRIOR APPLICATION DATA:
APPLICATION DATE: 02-JUN-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: MCKAy, Ronald D.G.
APPLICANT: Lendahl, Urban
APPLICANT: Lendahl, Urban
                                       REFERENCE/DOCKET NUMBER: 32,227
REFERENCE/DOCKET NUMBER: MIT-4641AAAA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk...
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                            APPLICATION NUMBER: US 07/180,548
ATTORNEY/AGENT INFORMATION
NAME: Granahan, Patricia,
REGISTRATION NUMBER: 32,227
                                                                                                                                                                                                         PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TLE OF INVENTION: Nestin Expression As An Indicator TLE OF INVENTION: Neurospithelial Tumors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         221 -ATLNOMLWCRLRELKDOGPPPSFLELMKVIREEEEEEASFENESIEEPEERDGY 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      123 LRLENYEROOQEVARLOAQVIKLOORCRMYGAETEKLOKQLASEKBIQMQLQEEETLPGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    172 RYLKTY---QEEGEKVSAYVLRLETLLR-----KAVEKRAIPRRIADQVRLEQVMAG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             183 QETLAEELRTSLRRMISD:-PVYFMERNYEMPRGDTSSLRYDFRYSEDREQVRGF 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             112 KEWPVTEAEKKRWLAESLRGPALDLMHIVQADNPSISVEECLEAFKQVFGSLESRRTAQV 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            44 PCDAPKLISQEALLHQ--HHCPQ--LEALQEKLRLL-----EENHQL-REEASQ--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       54 PCISPELLAH--LIGQAMAHAPQPLLPMRYRKLRVFSGSAVPAPEEESFEVWLEQATEIV 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 Similarity 22.6
53; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     B: Hamilton, Brook,
Two Militia Drive
: 617-861-6240
617-861-9540
OR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  U.S.A.
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22.6%; Pred. No. 0.27;
ative 40; Mismatches 85; Indels 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Smith & Reynolds,
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12

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; LENGTH: 1805 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-853-913-2
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Best Local Similarity
Matches 68; Conserv
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881
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                                                                                                                                                                                                                                                                                                                                                         664 PGAEDQMLERL----VEKEDQSFPRSPEEEDQEACRPLQKENQEPLGYEEAEGQILE---- 716
                                                                                                                                                                                                                                                                  717 -----RLIEKESQESIRSPEEEDQEAGRSLQKENQEPLGYEEAEDQMLERLIEKESQE 769
                                                                                                                                                                                                                                                                                                        75 PLLPMRYRKLRVFSGSAVPAPEEESFEVWLEQATEIVKEWPVTEAEK-----KRWLAS 127
                                                                                                                                                                                                                                                                                                                                                                                                 15 PNQDTEFLERLNLFLEKEGQTVSGMFRALGQEGVSPATVPCISPELLAHLLGQAMAHAPQ 74
IIIPQESETQVSLRPPEE--EDQRIVNHLEKESQEFSRSSEEEEQVMERSLEGB-NHE 935
                                          EKVSAYVLRLETLLRKAVEKRAIPRRIADQVRLEQVMAGATLNQMLWCRLRELKDQG--- 238
                                                                                                                                                                                                                        SLRGPALDLMHIVQADNPSISVEECLEAFKQVFGSLESRRTAQVRYLKTYQEEG----- 181
                                                                                         EKVS-----QDSLGSLAEENVQPLRYLEE---DDCINKSLLEDKTHKSLGSLEDRNGDS 880
                                                                                                                                                                                                                                                                                                                                                                                                                                              6.4%; Score 93; DB 1; Length 1805; ilarity 22.8%; Pred. No. 4.1; Conservative 35; Mismatches 137; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Search completed: April 8, 2005, 12:52:57 Job time: 23.7385 secs

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Result
                                                                                                                                                                                                                                                                                                                                                                       Database
                                                                                                                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match U%.
Maximum Match 100%.
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                         Minimum DB
Maximum DB
                                                                                                                                                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OM protein -
    Score
                                                                                                                                                                                                                                                                                    d. No. is the number of results predicted by chance to have a
re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                       seq length: 0 seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein search, using sw model
                                                                                                                                                                                                                                           Query
                                                                                                                                                                                                                                                                                                                   IBSUED PATENTS AA:*

1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*

2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-037-860-4
1729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BLOSUM62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  513545 segs, 74649064 residues
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    April
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Copyright
                                                                                                                                                                                                                                           Length DB. .ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8, 2005, 11:48:54; Search time 25.272 Seconds (without alignments) 971.808 Million cell updates/sec
   GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd
 SUMMARIES
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Sequence 4, Appli
Sequence 7, Appli
Sequence 7, Appli
Sequence 25, Appli
Sequence 2, Appli
Sequence 16406, A
Sequence 16406, A
Sequence 16406, A
Sequence 2, Appli
Sequence 2, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 11557, A
Sequence 11567, A
Sequence 11561, Appli
Sequence 32748, A
Sequence 11561, Appli
Sequence 32748, A
Sequence 31, Appli
Sequence 31, Appli
Sequence 2086, A
Sequence 23, Appli
Sequence 31, Appli
Sequence 31, Appli
Sequence 31, Appli
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SGAIRRQLWLTGAGEGPGPKPLSVAGADP 329

SGAIRRQLWLTGAGEGPGPKPLSVAGADP

301 301 241 241 181 181

**5** B 5

LEHTNEVLEEWQVSDVEKRRLMESLRGPAADVIRILKSNNPAITTAECLKALEQVFGSV

LEHTNEVLEEWQVSDVEKRRRLMESLRGPAADVIRILKSNNPAITTAECLKALEQVFGSV

300

240 180 180 120

240

120 60

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61 61

Oy 1 M	Query Match Best Local Simi Matches 329;	28 87 5.0 600 3 29 87 5.0 600 3 30 87 5.0 373 4 31 86.5 5.0 373 4 32 86 5.0 854 4.9 469 3 34 85 4.9 1209 469 3 36 85 4.9 1209 469 3 37 84.5 4.9 1209 406 4 39 84.5 4.9 486 6 49 40 84 4.9 486 6 41 83.5 4.8 332 4 42 83.5 4.8 341 1 43 83 4.8 341 1 44 83 4.8 524 3 45 83 4.8 341 1 47 83 527-4 88 4 8 524 3 48 83 4.8 529 3 49 87 88 83 4.8 529 3 49 87 88 83 4.8 529 3 49 87 88 83 4.8 529 3 49 87 88 83 4.8 529 3 40 84 89 87 89
AMTLLEDWCR	nilarity Conservat	F. H. W. Z.
GMDVNSQI 	100.0%; 100.0%; tive	600 3 US 600 3 US 1300 4 US 373 4 US 854 4 US 854 9 US 1105 3 US 4866 4 US 871 3 US 871 4 US 871 3 US 871 1 US
mamtlledwcrgmdvnsortllvwgipvncdeabibetloaampovsyrmlgrmfwrben 	; Score 1729; DB 3; Length ; Pred. No. 3.1e-182; 0; Mismatches 0; Indels	US-08-800-929A-12 US-09-617-053A-12 US-09-617-053A-12 US-09-328-352-7009 US-09-328-352-7009 US-09-314-000C-4673 US-09-410-372-9 US-09-252-991A-25844 US-09-252-991A-25844 US-09-328-352-6564 US-09-328-352-6564 US-09-328-352-6564 US-09-343-001C-3979 US-08-314-001C-3979 US-08-557-210A-3 US-08-557-210A-3 US-08-557-210A-4  ALIGNMENTS  ALIGNMENTS  1189527A  1189527A  1189527A  1189527A
VSYRMLGRME          VSYRMLGRME	329;	Sequence
WREEN 60	Gaps 0;	12, Appl 12, Appl 4501, Ap 7009, Ap 7009, Ap 7009, Appli 25844, A 2, Appli 6564, Ap 279, Ap 19, Appli 19, Appli 4, Ap 24064, A 254064, A 26564, Ap 25664, Ap 26564, Ap 26564, Ap 279, Ap 2979, Ap 2979, Ap 2055, Ap 19, Appli 4, Appli

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FILE REPERENCE: SLK98-01
CURRENT APPLICATION NUMBER: US/09/189,527A
CURRENT FILING DATE: 1998-11:30
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FRSUSEQ for Windows Version 3.0
SEQ ID NO 7
LENGTH: 195
TYPE: PRT
ORGANISM: homo sapiens
US-09-189-527-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 13, Application US/09189527A

Patent No. 6387639

GENERAL INFORMATION:
APPLICANT: Jerome B. Posner
APPLICANT: Josep O. Dalmau
APPLICANT: Josep O. Dalmau
TITLE OF INVENTION: Ma Family Polypeptides and Anti-Ma
TITLE OF INVENTION: Antibodies
FILE REFERENCE: SLK98-01
CURRENT APPLICATION NUMBER: US/09/189,527A
CURRENT FILING DATE: 1998-11-10
NUMBER OF SEO ID NOS: 14
SOFTWARE: FastSEQ for Windows Version 3.0
SECTION 13
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US-09-189-527-7
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; TYPE: PRT
; ORGANISM: homo sapiens
US-09-189-527-13
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                                                                                                                                                                                                                                                           Sequence 7, Application US/09189527A
PALENT NO. 6387639
GENERAL INFORMATION:
APPLICANT: Jerome B. Posner
APPLICANT: Josep O. Dalmau
APPLICANT: Myrna R. Rosenfeld
TITLE OF INVENTION: Ma Family, Polypeptides and
TITLE OF INVENTION: Antibodies
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 153; Conservative
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Best Local (
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43.2%; Score 747.5; DB 3;
Local Similarity 49.8%; Pred. No. 1.7e-73;
hes 153; Conservative 49; Mismatches 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     304 IRRQLWL 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     244 RDAQIKELNTYQNPGEKLSAYVIRLEPLLQKVVEKGAIDKDNVNQARLEQVIAGANHSGA 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 DTNCSAPRYTISPEFWTWĄQTĽGAAVQPĽLEQMLÝRELRVFSGNTISIPGALAFDAWLEH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      126 QNPTPTPGPEMPAEMLNY, ILDNVIQPLVESIWYKRLTLFSGKGHPRAWRGNFDPWLEH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QDWCRGEHLNTRRCMLILGIPEDCGEDEFEETLQEACRHLGRYRVIGRMFRREENAQAIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LRDKLKL 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTEMLOMWOVPEGEKRRIMECLRGPALOVVSGLRASNASITVEECLAALOOVFGPVESH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LELAQDIDYALLPREIPGKGGPWEVIVKPRNSDGEFLNRLNRFLEEERRTVSDMNRVLGS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LELTGAVDYAAIPREMPGKGGVWKVLFKPPTSDAEFLERLHLFLAREGWTVQDVARVLGF 125
25.5%; Score 441; DB 3; 46.4%; Pred. No. 3e-40;
                     Length 195;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 462;
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US-09-902-540-16701
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APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
APPLICANT: Wegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof FILE REFERENCE: 38-10(1.5849)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 16701
LENGTH: 551
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                            y Match
6.4%; Score 110.5; DB 4;
Local Similarity 21.5%; Pred. No. 0.0056;
hes 71; Conservative 47; Mismatches 113;
348
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                                                                                                                                              237
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                               295 IAGANHSGAIRRQLWLTGAGEGPGPKPLSV 324
                                                                                                         236 VFGSVESSRDAQIKFLNTYQNPGEKLSAYVIRLEPLLQKVVEKGAIDKDNVNQARLEQV- 294
                                                                                                                                                                                176 NFDPWLEHTNEVLEEWQVSDVEKRRRLMESLRGPAADVIRILKSNNPAITTAECLKALEQ 235
                                                                                                                                                                                                                     187 LDAESVAWLEQALKEYKGTIVCITHDRYFLDNAAEWILE-----LDRGEGVP--WKG
                                                                                                                                                                                                                                                                                               127 DAVNGWELDRTIEMAMDALRLPPGDADVTKLSGGEKRRVALCRILLEKPDLLLLDEPTNH 186
                                                                                                                                                                                                                                                                                                                                 178 DPWLEHTNEVLEEW 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  122 ALGQEALSPATVPCISPELLAHLLGQAMAHAPQPLL-PMRYRKLRVFSGSAVPAPEEESF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    122 VLGFQ--NPTPTP--GPEMPAEMLNYILDNVIQPLVESIWYKRLTLFSGKGHPRAWRGNF 177
                                                                                                                                                                                                                                                                                                                                                                                                                                          71;
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                                                                                                                                                                                                                                                                                                                                                                                                         60 NAKAALLELTGAVDYAAIPREMPGKGGVWKVLFKPPTSDAEFLERLHLFLARE------ 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62 NAVLLELLEDTDVSAIPSEVQGKGGVWKVIFKTPNQDTEFLERLNLFLEKEGQTVSGMFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62 KAALLELTGAVDYAAIPREMPGKGGVWKVLFKPPTSDAEFLERLHLFLAREGWTVQDVAR 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            90;
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                                                                                                                                              NYSSWLEOKOKRLELEEKSESHROKTLKREL----EWVRASPKAROAKSKAR-IAAYEE
                                                                                                                                                                                                                                                                                                                                                                      NVELGLKEIRATLDRF---NEVSAK-----FAEPMSDAE-MEKL---LAEQGRLQDAI 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EVWLEQATEIVKEW
                                                                      LLNQTQDKRDATGEVIIP---PGPQLGGLVVEAKGLRKAYGDRLLIEDLNFKLPRGGIVG
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RESULT 5 US-09-914-259-25

Sequence 25, Application US/09914259

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784

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APPLICANT: Hyman, Paul
APPLICANT: Hyman, Paul
APPLICANT: Hyman, Paul
APPLICANT: Hyman, Mark
APPLICANT: Williams, Mark
ITILE OF INVENTION: STAGED ASSEMBLY OF NANOSTRUCTURES
FILE REFERENCE: 8471-010-999
CURRENT APPLICATION NUMBER: US/09/914,259
CURRENT FILING DATE: 2000-11-21
NUMBER OF SEQ ID NOS: 180
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 25
LENGTH: 935
                                                                                                                                                                                                           Sequence 2, Application US/09365590

Patent No. 6187563

GENERAL INFORMATION:
APPLICANT: 8014mens, Michale
TITLE OF INVENTION: INTERACTING POLYPEPTIDES FOR
TITLE OF INVENTION: AUTOANTIGENS OF AUTOIMMUNE DISE;
PILE REFERENCE: 01918-200 (CCR-941)
FULE REFERENCE: 01918-200 (CCR-941)
CURRENT APPLICATION NUMBER: US/09/368,590
CURRENT FILING DATE: 1999-08-04
EARLIER APPLICATION NUMBER: 60/095,657
EARLIER APPLICATION NUMBER: 60/095,657
EARLIER FILING DATE: 1998-08-07
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 3.0

SEO ID NO 2
LENGTH: 2293
TYPE: PRT
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, ORGANISM: Syncephalastrum racemosum
US-09-914-259-25
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                                                                                                                                                                       ; ORGANISM: Human
US-09-368-590-2
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Best Local Similarity
Matches 69; Conserv
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GENERAL INFORMATION:
                                                                                                                       Query Match
                                                                         Matches
                                                                                                   Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           352 KSEAVTYQTYIAALEGEVNVWRTGGTVP------EGKWVTMDKVSKGDFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         297 NSRTTLIINCSPSSYNEAETLSTLRFGARAKSIKNKAKV----NADLSPAELKALLKKV 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16 NSQRTLLVWGIPVNCDEAEIEETLQAAMPQVSYRMLGRMFWREENAKAALLEL-----
9 WCRGMDVNSQR-----TLLVWGIPVNCDE--AEIEETLQAAMPQVSYRMLGRMFWREEN
                                                                         78; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GSVESSRDAQIKFLNTYQNPGEKLSAYVIRLEPLLQKV--VEKGAIDKDNVNQ--ARLEQ 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VIAGANHSGAI --- RROL 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LMD--QISEKETELTNREKLLESLREEMGYYKEQEQSVTKENQQMTSELSELRLQLQKV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VLEEWQVSDVE----KRRRLMESTR---GPAADVIRILKSNNPAITT--AECLKALEQVF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -SYESKENAIT--VDSLKEANQDLMAELEELKKNLSEMRQAHKDATDSDKEKRKAEKMAQ 549
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6.0%; Score 103; DB 4; Length 935; 21.7%; Pred. No. 0.091;
                                                                       5.8%; Score 100.5; DB 3; 22.6%; Pred. No. 0.76; ive [51; Mismatches 139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 56; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DISEASES
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                                                                              Indels
                                                                                                                       Length
                                                                                                                               2293;
                                                                              77;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 60/241.755
PRIOR PILING DATE: 2000-10-20
PRIOR PELICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR PILING DATE: 2000-09-08
PRIOR PILING DATE: 2000-09-08
PRIOR PILING DATE: 2007012
SOPTWARE: FastSEQ for Windows Version 4.
SEQ ID NO 7309
LENGTH: 2600
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US-09-949-016-7309
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF PILE REFERENCE: CLOOL307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION.
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Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Match 5.8%; Score 99.5; DB 4; Local Similarity 22.6%; Pred. No. 1.2; Nes 78; Conservative 50; Mismatches 140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    1005 WNRIVELVEORKEEMSAVILVENHVLEVAEVRAQVREKRRAV--BSAPRAGGALQWRLSG 1062
                                                       1234 AHIYQLFLR-DLRQALVVI;RNQEMALSGAELPGTVESVEEALKQHRD---
                                                                                                                                                                                                                                                        1123 AGRLQRFLHDLDAFL---DWLVRAQEAAGGSEGFLPNSLEEADALLARHAALKEEVDQRE 1179
                                                                                                                                                                                                                                                                                                                                                      1063 LEAALQALEPRQAALLEEAALLAERFPAQAARLHQGAEELGAEWGALASAAQACGEAVAA 1122
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                                                                                                                                                                                                                                                                                                                                                                                                    61 AKAALLEL----TGAVDYAAIPRE-MPGK-----GGVWKVLFKPPTSDAE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9 WCRGMDVNSQR------TLLVWGIPVNCDE--AEIEETLQAAMPQVSYRMLGRMFWREEN 60
                                                                                                                                                                                                                                                                                                    -----FLERLHLFLAREGWTVQDVARVLGFQNPTPTPGPEMPAEMLNY-ILDNVIQPLV 153
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                                                                                                                                                          ED--YARIVAASEALLAADGAELGPGLALDEWLPHLELGWHKLLGLWEA----RREALVO
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                                                                                                          S-----LRGPAADVIRILKSNNPAITTAECLKALEQVFGSVESSRDAQIKFLNTYQNPG 258
                                                                                                                                                                                                        ESIWYKRL----TLFSGKGHPRAWRGNFDPWLEHT----NEVLEEWQVSDVEKRRLME 204
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               -- QKVVEKGAIDKDNVNQARLEQ 293
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US-09-902-540-16406
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US-09-489-039A-12764
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PRIOR PILING DATE: 199-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 12764
LENGTH: 288
                                   NUMBER C. SEQ ID NO 16406
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Matches
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                                                                                                                                    APPLICANT: Goldman, Barry S. APPLICANT: Hinkle, Gregory J. APPLICANT: Hinkle, Gregory J. APPLICANT: Slater, Steven C. APPLICANT: Wiegand, Roger C. APPLICANT: Wiegand, Roger C. TITLE OF INVENTION MYXOCOCCUB xanthus Genome Sequences and Uses Thoreof FILE REFERENCE: 38-10 (15849)B: CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2004061
                                                                            PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
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                      TYPE: PF
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ORGANISM: Myxococcus xanthus:
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              APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Wiegand, Roger C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Secritize Reference: 38-10 (15849) B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
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US-09-328-352-6016
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                                                                                                                                                                                                  GENERAL INFORMATION:
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SEQ ID NO 6016
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APPLICANT: GATY L. Breton et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                   Sequence 15988, Application US/09902540 Patent No. 6833447
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CURRENT FILING DATE: 1999-06-04
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les 52; Conserva
    FILING DATE:
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ilarity 27.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 93.5; DB 4;
Pred. No. 0.46;
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                                                                                                 Sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 573;
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61;

Gaps

335

294

244

Gaps

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; ORGANISM: Myxococcus
US-09-902-540-15988
                                                                                                                                                                    COUNTAIL
ZIP: 22040-0747
ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk-
MEDIUM TYPE: Ploppy disk-
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC COMPATION SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1
CURRENT APPLICATION DATA:

"PRITTATION NUMBER: US/07/320,281C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application Patent No. 5739026
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
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LENGTH: 2214
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             FILING DATE: 13-AUG-1992.
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MUTPHY JT., Gerald M.
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 828-103P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-241-1300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITILE OF INVENTION: DNA Expression Systems Based
TITILE OF INVENTION: Alphaviruses
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Garott, Henrik
APPLICANT: Liljestrom, Peter
                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
STREET: P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 720 -GVAASLLARAASLASEPLPL 739
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  76 AIPREMPGKGGVWKVLFKPPTSDAEFLERLHLFLAREGWTVQDVARVLGFQNP--TPTPG 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25 GIPVNCDEAEIEETLQAAMPQVSYRMLGRMFWREENAKAALLELTGAV------DYA
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T: P.O. Box 747
Palle Church
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Application US/07920281C
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21.0%; Pred. No. 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/08466277 Patent No. 6190666 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 5.3%; Score 92.5; DB 1; Best Local Similarity 19.6%; Pred. No. 6.4; Matches 74; Conservative 50; Mismatches 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
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                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,277
APPLICATION COMBER: 06-Jun-1995
FILING DATE: 06-Jun-1995
                                                                                                                                                                                      ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                  FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: DNA Expression Systems
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1013
                                                                                      PRIOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Garoff, Henrik
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       110 -AREGWTVQDVARVLGFQNPTPTPGPEMPAEMLNYILDNVIQPLVESIWYKRLTLFSGKG
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                                                                                                                                                                                                                                                                                                                                          STREET: P.O. Box 7
CITY: Falls Church
STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SVLDNVIPINRRLPHALVAEYKTVKGSRVEWLVNKVRGYHVLLVSEYNLALPRRRVTWLS
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                                                             APPLICATION NUMBER: 07/920,281
                                                                                  CLASSIFICATION: <Unknown>
APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
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Gerald M.
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                                                                                                                                                                                                                                                                                                                                                                                                               Kolasch & Birch
                                                                                                                                                                                               Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Based
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TOPOLOGY: linear;
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MOLECULE TYPE: protein
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SEQUENCE DESCRIPTION: SEQ ID NO:
US-08-466-277-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-688-842-2
Sequence 2, Application US/09688842
Patent No. 6770283
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 19.6%; .Pred. No. 6.4; Matches 74; ,Conservative 50; Mismatches 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local
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TELEFAX: 703-241-2848
TELEX: 248345
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 231 amino acids
                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Birch, Stew
STREET: P.O. Box 747
CITY: Falls Church
STATE: Virginia
COUNTRY: USA
ZIP: 22040-0747

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/688,842

FILING DATE: 17-Oct-2000
                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: DNA Expression Systems Based
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1193 ------PLNVTGAD 1200
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REFERENCE/DOCKET NUMBER: 828-103P
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Garoff, Henrik
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1013 NVCWAKSLVPVLDTAGIRLTAEEWSTIITAFKEDRAYSPVVALNEICTKYYGVDLDSGLF 1072
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           865 GKWRTTNPCNKPIIIDTTG------QTKPKPGDIVLTCFRGWAKQLQLDYRGHEVMTA 916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        52 GRMFWREENAKAALLELTGAVDYAAIPREMPGKGGVWKVLFKPPTSDAEFLERLHLFL-- 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SVLDNVIPINRRLPHALVAEYKTVKGSRVEWLVNKVRGYHVLLVSEYNLALPRRRVTWLS 1192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----ECLKALEQV-----IRILKSNNPAITTA-----ECLKALEQV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AASOGLTRKGVYAVROKVNENPLYAP--ASEHVNVLLTRTEDRLV----WKTLA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----GDPWIKVLSNIPQGNFTATLEEWQ----EEHDKIMKVIEGPAAPVDAFQNKA 1012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5.3%; Score 92.5; DB 3; Length 2431; 19.6%; Pred. No. 6.4;
                                                                                                                                                                                                                                                                                                                                                                               Alphaviruses
                                                                                                                                                                                                                                                                                                              Stewart, Kolasch & Birch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----FGSVESSR-DAQIKFLNTYQNPGEKLSAYVIRLEPL 271
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US-09-055-097-1
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                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Guegler, Karl J.
APPLICANT: Corley, Neil C.
APPLICANT: Shah, Purvi
                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/09055097
Patent No. 5955282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 5.3%;
Best Local Similarity 19.6%;
Matches 74; Conservative 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEX: 248345
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                           TITLE OF INVENTION: HUMAN OXIDIZED LDL RECEPTOR NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                               APPLICANT:
                             ADDRESSEE: Incyt
STREET: 3174 Por
CITY: Palo Alto
STATE: Californi
COUNTRY: USA
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REFERENCE/DOCKET NUMBER: 82
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-241-1300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/466,277
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1073 SAPKVSLYYENNHWDNRPGGRMYGFNAATAARLEARHTFLKGQWHTGKQAVIAERKIQPL 1132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1133 SVLDNVIPINRRLPHALVAEYKTVKGSRVEWLVNKVRGYHVLLVSEYNLALPRRRVTWLS 1192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         312 GAGEGPGPKPLSVAGAD 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   272 --LQKVVE-------KGAIDKDNVNQARLEQVIAGANHSGAI--RRQLWLT 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            169 HPRAWRGNFDPWLEHTNEV------LEEWQVSDVEKRRLMESLRGPAADV------
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         94304
                                                      California
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                                                                                              E: Incyte Pharmaceuticals,
3174 Porter Drive
                                                                                                                                                                                                                 Patterson, Chandra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1200
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CLASSIFICATION:
CLASSIFICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
AREGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: 29,132
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Search completed: April 8, 2005, 12:52:53
Job time: 27.272 secs
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OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/055,097
FILING DATE: Filed Herewith
CLASSIFICATION:
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MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                  217 LKSNNPAITTAECLK 231
                                                                                                                                                                                                                                                                                                                                            252 -----PHTW-GPFPPYASGTGYVLSASAVQLILKVASRAPLL-----PLEDVFVG 295
                                                                                                                                                                                                                                                                                                                                                                                                                             160 RLTLFSGKGHPRAWRCHFDPWLEHTNEVLEEWQVS---DVEKRRRLMESLRGPAADVIRI 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   218 HSEEVPLLYLGRVHWRV-----NESRTPGGR-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               106 H-----LFLAREGWTVQDVARVLGFQNPTPTPGPEMPAEMLNYILDNVIQPLVESIWYK 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             158 LWAEKHCPMARYVLKTDDDVYVNVPELVSELVLRGGRWGQWERSTEPQRBAEQEGGQVL 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    101 RGLRVQTLFLLGEPNAQHP---VWGSQGSDLASESAAQGDILQAAF-QDSYRNLTLKTLSG
                                                                                                                                                                          296 VSARRGGLAPTQCVK 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              54 MFWREENAKAALLELTGAVD-YAAIPREMP-----GKGGVWKVLFKPP-TSDAEFLERL 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11 RGMDV------NSQRTLLVW---GIPVNCDEAEIBETLQAAMPQVSYR-----MLGR 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   89; Indels 79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ------HRVSEEQW-- 251
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Result
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Maximum Match 1,00%
Listing first 45 s
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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887.5
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Gapop 10.0 , Gapext 0.5
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1729
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    Stand
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           / Ggn2 6/ptodatta/1/pubpaa/USO6_REW_PUB_pep.*
/ Ggn2 6/ptodatta/1/pubpaa/USO6_PUBCOMB.pep.*
/ Ggn2 6/ptodatta/1/pubpaa/USO7_NEW_PUB_pep.*
/ Ggn2 6/ptodatta/1/pubpaa/USO7_NEW_PUB_pep.*
/ Ggn2 6/ptodatta/1/pubpaa/USO8_NEW_PUB_pep.*
/ Ggn2 6/ptodatta/1/pubpaa/USO8_PUBCOMB.pep.*
/ Ggn2 6/ptodatta/1/pubpaa/USO8_PUBCOMB.pep.*
/ Ggn2 6/ptodatta/1/pubpaa/USO8_PUBCOMB.pep.*
/ Ggn2 6/ptodatta/1/pubpaa/USO9_PUBCOMB.pep.*
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/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*
                                                                                                                                                                                                   13 US-10-037-860-4
10 US-09-804-014A-40
9 US-09-965-529-7
10 US-09-969-680A-7
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9 US-09-965-529-1
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    10 US-09-804-014A-16

10 US-09-969-680A-1

10 US-10-341-434-1

10 US-10-341-43-7

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10 US-09-804-014A-74

13 US-09-804-014A-74

13 US-10-408-765A-238
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<u>.</u>	-10-	-10-282-1227	-10-329-079-1	-10-408-765A-1	-10-425-114-5	-10-437	-370	10-080-608A-2	-10-282-122	09-738-6	-10-282-122A-4	-10-369-493-179	-10-282-122A-6	-10-282-122A-65	0-282-122A-50	-10-282-122A-49	-10-329-079	-10-221-278-35	-10-291-172	-10-408-765A-29	US-09-864-761-34645	37-860	-10-029-386-337	-10-296-115-12	US-10-959-539-26	-10-094-466	-09-804-014A-4	-09-	-10-037-860-	-10-037-860-	US-10-094-749-1978
Sequence 10509, A	2, 2		e 11,	101	509	144	Sequence 114, App	25,	e 584	Sequence 5485, Ap	Sequence 47973, A	Sequence 17979, A	Sequence 66072, A	Sequence 65151, A	Sequence 50770, A	Sequence 49641, A	Sequence 45, Appl	Sequence 355, App	Sequence 355, App		Sequence 34645, A	Sequence 9, Appli	33	12	26	38	e 42	e 41	e 7,	equence 11,	Sequence 1978, Ap

## ALIGNMENTS

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APPLICANT: LI, LI
APPLICANT: LI, LI
APPLICANT: Vernet, Corine
APPLICANT: Vernet, Corine
APPLICANT: Shimkets, Richard
APPLICANT: Spaderna, Steven
APPLICANT: Majunder, Kunud
TITLE OF INVENTION: NOVel Polypeptides and Nucleic Acids Enco
FILE REFERENCE: 19966-721, US
CURRENT FILING DATE: 2002-03-24
PRIOR APPLICATION NUMBER: 60/188, 316
PRIOR FILING DATE: 2000-03-10,
PRIOR APPLICATION NUMBER: 60/189, 139
PRIOR APPLICATION NUMBER: 60/189, 139
PRIOR APPLICATION NUMBER: 60/189, 140
PRIOR FILING DATE: 2000-03-14
PRIOR APPLICATION NUMBER: 60/190, 401
PRIOR FILING DATE: 2000-03-14
PRIOR FILING DATE: 2000-03-17
PRIOR APPLICATION NUMBER: 60/190, 231
PRIOR FILING DATE: 2000-03-17
PRIOR APPLICATION WUMBER: 60/190, 231
PRIOR FILING DATE: 2000-03-17
PRIOR FILING DATE: 2000-03-17
PRIOR APPLICATION Specification
US-09-804-014A-40

US-09-804-014A-40

PRIOR APPLICATION: Wherein Xaa is any amino acid as defined
OTHER INFORMATION: wherein Xaa is any amino acid as defined
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US-09-804-014A-40
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Best Local Simi:
Matches 317;
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                                                                 ESSRDAQIKFLNTYQNPGEKLSAYVIRLEPLLQKVVEKGAIDKDNVNQARLEQVIAGANH 300
                    RVLGFQNPTPTPGPEMPAENILNYILDNVIQPLVESIWYKRLTLFSGKGHPRAWRGNFDPW
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RVLGFQNPTPTPGPEMPAEMLNYILDNVIQPLVESIWYKRLTLFSGKGHPRAWRGNFDPW
                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                    96.4%; Score 1666; DB 10;
99.7%; Pred. No. 2.7e-154;
59.7%; Mismatches 1;
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: YUE, Henry
APPLICANT: TANG, Y. Tom
APPLICANT: BURFORD, Neil
APPLICANT: BURFORD, Neil
APPLICANT: BAYDMAN, Olga
APPLICANT: BAYDMAN, Olga
APPLICANT: BAYDMAN, Olga
APPLICANT: BAYDMAN, Ariah R.
APPLICANT: DATTERSON, Chandra
TITLE OF INVENTION: MEMBRANE ASSOCIATED PROTEINS
FILE REFERENCE: PP-0731 USA
CURRENT APPLICATION NUMBER: US/09/965,529
CURRENT FILING DATE: 1999-08-17; 1999-11-09; 2000-08-14
NUMBER OF SEQ ID NO 7
SOFTWARE: PERL PROGram
SEQ ID NO 7
SEQ ID NO 7
SEQ ID NO 7
TYDE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID NO. US20020182671A1 2483172CD1
US-09-965-529-7
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Best Local Similarity
Matches 308; Conserv
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                                           SGAIRRQLWLTGAGEGPGP
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Pred. No. 5.8e-148;
1; Mismatches 10;
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APPLICANT: BURFORD, Neil; AZIMZAI, Yalda
APPLICANT: BUGHN, Mariah R.; LU, Dyung Aina M.
APPLICANT: PATTERSON, Chandra
TITLE OF INVENTION: MEMBRANE ASSOCIATED PROTEINS
FILE REFERENCS: PF-0731-1 USA
CURRENT APPLICATION NUMBER: US/09/969,680A
CURRENT FILING DATE: 2001-10-02
PRIOR APPLICATION NUMBER: US/09/22315
PRIOR APPLICATION NUMBER: 60/149,641
PRIOR APPLICATION NUMBER: 60/149,641
PRIOR FILING DATE: 1999-08-17
PRIOR FILING DATE: 1999-08-17
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                                                                                  GENERAL INFORMATION:
APPLICANT: Li, Li
APPLICANT: Padigaru,
APPLICANT: Vernet,
APPLICANT: Fernandes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 7, Application US/09969680A Publication No. US20030124649A1 GENERAL INFORMATION:
                                                                                                                                                                                   Sequence 39, Application US/09804014A Publication No. US20030064489A1
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Best Local Similarity
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NUMBER OF SEQ ID NOS: '
SOFTWARE: PERL Program
                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. US20030124649A1 2483172CD1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: 60/164,203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
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        AVT: Padigaru, Muralidhara
AVT: Vernet, Corine
AVT: Fernandes, Elma
AVT: Shimkets, Richard
AVT: Spaderna, Steven,
AVT: Majumdor, Kunud
DF INVENTION: Novel Polypeptides a
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            and Nucleic Acids Encoding
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GENERAL INFORMATION:

APPLICANT: LAL, Preeti
APPLICANT: YUE, Henry
APPLICANT: TANG, Y. Tom
APPLICANT: TANG, Y. Tom
APPLICANT: BANDMAN, Olga
APPLICANT: BANDMAN, Olga
APPLICANT: BAUGHN, Mariah R.
APPLICANT: LU, Dyung Aina M.
APPLICANT: PATTERSON, Chandra
ITITLE OF INVENTION: MEMBRANE ASSOCIATED PROTEINS
ITITLE OF INVENTION MEMBRANE ASSOCIATED PROTEINS
ITIE REFERENCE: PF-0731 USA
CURRENT APPLICATION NUMBER: 05/04/965,529
CURRENT APPLICATION DATE: 2001-09-26
PRIOR APPLICATION DATE: 2001-09-26
PRIOR APPLICATION DATE: 1999-08-17, 1999-11-09, 2000-08-14
NUMBER OF SEQ ID NOS: 74
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US-09-965-529-1
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Publication No. US20020182671A1
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FILE REFERENCE: 15966-721 US
CURRENT FILING DATE: 2002-04-24
PRIOR APPLICATION NUMBER: 60/188,316
PRIOR FILING DATE: 2000-03-10
PRIOR FILING DATE: 2000-03-10
PRIOR FILING DATE: 2000-03-10
PRIOR PILING DATE: 2000-03-10
PRIOR APPLICATION NUMBER: 60/189,139
PRIOR APPLICATION NUMBER: 60/189,139
PRIOR PILING DATE: 2000-03-14
PRIOR PILING DATE: 2000-03-14
PRIOR PILING DATE: 2000-03-14
PRIOR PILING DATE: 2000-03-17
PRIOR APPLICATION NUMBER: 60/190,401
PRIOR APPLICATION NUMBER: 60/190,401
PRIOR PILING DATE: 2000-03-17
PRIOR APPLICATION NUMBER: 60/190,231
PRIOR PILING DATE: 2000-03-17
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Best Local Similarity 55.4%;
Matches 179; Conservative 53
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AGAVHK-TIRRELNLPEDGPAPG
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FILE REFERENCE: 15966-721 US:
CURRENT APPLICATION NUMBER: US/09/804,014A
CURRENT FILING DATE: 2002-04-24
PRIOR APPLICATION NUMBER: 60/188,316
PRIOR APPLICATION NUMBER: 60/188,316
PRIOR APPLICATION NUMBER: 60/189,277
PRIOR APPLICATION NUMBER: 60/189,277
PRIOR FILING DATE: 2000-03-10.
PRIOR FILING DATE: 2000-03-10.
PRIOR APPLICATION NUMBER: 60/189,139
PRIOR FILING DATE: 2000-03-14.
PRIOR APPLICATION NUMBER: 60/189,140
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; OTHER INFORMATION: Incyte ID No. US20020182671A1 112301CD1
US-09-965-529-1
                                        NUMBER OF SEQ ID NOS: 75
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 16, Application US/09804014A Publication No. US20030064489A1
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APPLICANT: Pad
APPLICANT: Ver
APPLICANT: Fer
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Best Local Similarity
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                                                                                                   PRIOR APPLICATION NUMBER: 60/190,401
PRIOR FILING DATE: 2000-03-17
PRIOR APPLICATION NUMBER: 60/190,231
PRIOR FILING DATE: 2000-03-17:
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ORGANISM: Homo sapiens
FEATURE:
   ORGANISM: Homo sapiens
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Majumder, Kumud
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; LENGTH: 351
; TYPE: PRT
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FEATURE:

NAME/KEY: misc_feature

OTHER INFORMATION: Incyte ID No. US20030124649A1 112301CD1

US-09-969-680A-1
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CURRENT FILING DATE: 2001-10-02
PRIOR APPLICATION NUMBER: US00/22315
PRIOR FILING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: 60/149,641
PRIOR APPLICATION NUMBER: 60/164,203
PRIOR FILING DATE: 1999-08-17
PRIOR APPLICATION NUMBER: 60/164,203
PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 74
SOFTWARE: PERL Program
                                                          Query Match
Best Local Similarity 55.4
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Best Local Similarity
Matches 179; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: LAL, Preeti; YUE, Henry
APPLICANT: TANG, Y. Tom; BANDMAN, Olga
APPLICANT: BURFORD, Neil; AZIMZAL, Yalda
APPLICANT: BAUGHN, Mariah R.; LU, Dyung Aina M.
APPLICANT: PATTERSON, Chandra
TITLE OF INVENTION: MEMBRANE ASSOCIATED PROTEINS
FILE REFERENCE: PF-0731-1 USA
                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
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MTLRLLEDWCRGMDMNPRKALLIAGISQSCSVAEIEEALQAGLAPLGEYRLLGRMFRRDE
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Pred. No. 5.5e-78;
53; Mismatches 84
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Pred. No. 5.5e-78;
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Sequence 10, Application US/10341434

Publication No. US20030215835Ai

GENERAL INFORMATION;
APPLICANT: OriGene Technologies

FITTE OF INVENTION: Differentially Regulated Prostate Cancer Genes

FILE REFERENCE: 9U 204 205 R1

CURRENT APPLICATION NUMBER: US/10/341,434

CURRENT FILING DATE: 2003-07;18

PRIOR APPLICATION NUMBER: US 60/348,164

PRIOR FILING DATE: 2002-01-15

PRIOR FILING DATE: 2002-01-15

INUMBER: OF SEG ID NOS: 238

SOFTWARE: Patentin version 3.1

SEG ID NO 10

CRGANISM: Homo Sapiens
RESULT 10
US-09-804-014A-73
; Sequence 73, Application US/09804014A
; Publication No. US20030064489A1
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US-10-341-434-10
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PRIOR FILING DATE: 2000-03-10
PRIOR PPLICATION NUMBER: 60/188,277
PRIOR PPLICATION NUMBER: 60/189,139
PRIOR APPLICATION NUMBER: 60/189,139
PRIOR PRIOR PRIOR APPLICATION NUMBER: 60/189,140
PRIOR PILING DATE: 2000-03-14
PRIOR APPLICATION NUMBER: 60/190,401
PRIOR APPLICATION NUMBER: 60/190,401
PRIOR APPLICATION NUMBER: 60/190,231
PRIOR APPLICATION NUMBER: 60/190,231
PRIOR PILING DATE: 2000-03-17
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US-09-804-014A-74
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                                      APPLICANT: Li, Li
APPLICANT: Padiga
APPLICANT: Vernet:
APPLICANT: Fernanc
APPLICANT: Shimket
APPLICANT: Spader:
                                                                                                                                                              Sequence 74, Application US/09804014A Publication No. US20030064489A1 GENERAL INFORMATION:
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APPLICANT: Padiga
APPLICANT: Vernet
APPLICANT: Fernan
APPLICANT: Shimke
APPLICANT: Spader
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APPLICANT: Majumder, Kumud
TITLE OLIVENTION: Novel Polypeptides and Nucleic Acids Encoding
FILE REFERENCE: 15966-721 US
CURRENT APPLICATION NUMBER: US/09/804,014A
CURRENT FILING DATE: 2002-04-24
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ORGANISM: Homo sapiens
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Fernandes, Elma
Shimkets, Richard
Spaderna, Steven
Majumder, Kumud
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Shimkets, Richard
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; Pred. No. 8.7e-77
53; Mismatches 7
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APPLICANT: Jerome B. Posner
APPLICANT: Myrna R. Rosenfeld
APPLICANT: Myrna R. Rosenfeld
TITLE OF INVENTION: Ma FAMILY POLYPEPTIDES ANI
TITLE OF INVENTION: ANTENDIES
FILE REFERENCE: 2581.104-1004.
FURRENT APPLICATION NUMBER: US/10/037,860
CURRENT FILING DATE: 2001-01-04
PRIOR APPLICATION NUMBER: 09/189,527
PRIOR FILING DATE: 1998-11-10
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FASTSEQ for Windows Version 4.0
SEG ID NO 13
LENGTH: 463
TYPE: PRT
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-804-014A-74
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PRIOR FILING DATE: 2000-03-10...
PRIOR APPLICATION NUMBER: 60/189,139
PRIOR APPLICATION NUMBER: 60/189,140
PRIOR APPLICATION NUMBER: 60/189,140
PRIOR FILING DATE: 2000-03-17
PRIOR APPLICATION NUMBER: 60/190,401
PRIOR APPLICATION NUMBER: 60/190,401
PRIOR FILING DATE: 2000-03-17
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Best Local S
Matches 175
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NUMBER OF SEQ ID NOS: 75
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PRIOR FILING DATE: 2000-03-10
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CURRENT FILING DATE: 2002-04-24
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S0.6%; Ecore 874.5; DB 1
Similarity 55.9%; Pred. No. 8.7e-77;
75; Conservative 53; Mismatches 78
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APPLICANT: Ghosh, Soumitra S.
APPLICANT: Faby, Eoin D.
APPLICANT: Zhang, Bing
APPLICANT: Zhang, Bing
APPLICANT: Zhang, Bindford W.
APPLICANT: Taylor, Steven W.
APPLICANT: Taylor, Steven W.
APPLICANT: Warnock, Dale E.
TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
TITLE OF INVENTION: DENTIFIED IN THE MITOCHONDRIAL PROTEOME
FILE REFERENCE: 660088.465
FILE REFERENCE: 660088.405
CURRENT APPLICATION NUMBER: US/10/408,765A
CURRENT FILING DATE: 2003-04-04
NUMBER OF SEQ ID NOS: 3077
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2385
LENGTH: 452
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US-10-408-765A-2385
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Best Local Similarity
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Best Local Similarity
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                                                                      NAKAALIBLIGAVDYAAIPREMPGKGGVWKVLFKPPTSDAEFLERLHLFLAREGWTVQDV 119
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                                ARVIGFONPTPTPGPEMPAEMLNYILDNVIQPLVESIWYKRITLFSGKGHPRAWRGNFDP 179
                                                                                                                                                  MALTILEDWCKGMDMDPRXALLIVGIPMECSEVEIQDTVKAGLQPLCAYRVLGRMPRRED
                                                                                                                                                                      MAMTLLEDWCRGMDVNSQRTLLVWGIPVNCDEAEIEETLQAAM-PQVSYRMLGRMFWREE
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ARALGC---CSLPAESLDAEVMPQVRSPPLEPPKESMWYRKLKVFSGTASPSPGEETFED 181
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nilarity 46.0%;
Conservative 64
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                                                                                                                                                                                                                        ; Score 744; DB 16;
; Pred. No. 9.1e-64;
64; Mismatches 100;
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APPLICANT: OYOSHIKAWA, TSUTOMU,
APPLICANT: OYSUKA, MOTOYUKI:
APPLICANT: NAGAHARI, KENJI
APPLICANT: NAGAHARI, KENJI
APPLICANT: MASUHO, YASUHIKO
TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA
FILE REFERENCE: 084335/0160
CURRENT APPLICATION NUMBER: US/10/094,749
CURRENT FILING DATE: 2002-03-12
PRIOR APPLICATION NUMBER: 60/350,435
PRIOR FILING DATE: 2002-01-24
PRIOR FILING DATE: 2002-01-24
PRIOR FILING DATE: 2002-01-24
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US-10-094-749-1978
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; ORGANISM: Homo sapiens
US-10-094-749-1978
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PRIOR FILING DATE: 2001-09-14,
NUMBER OF SEQ ID NOS: 3381
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1978
LENGTH: 399
                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
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                                                                                 121 SVÁGALG------VGLRRVCWLRSIGQAVQÞWÝEÁVRCQSLGVÉSGRDQÞAÞGEB 169
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235 QVFGSVESSRDAQIKFLNTYQNPGEKLSAYVIRLEPLLQKVVEKGAIDKDNVNQARLEQV
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SUGIYAMA, TETSUJI
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                                                 NPDPWLEHTNEVLEEWQ-VSDVEKRRIMESLRGPAADVIRILKSNNPAITTAECLKALE 234
                                                                                                                                                                  SFEVWLDHTTEMLHVWQGVSERERRRLLEGLRGTALQLVHALLAENPARTAQDCLAALA
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IRIE, RYOTARO
TAMECHIKA, ICHIRO
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40.9%; Pred. No. 1.1e-51;
tive 64; Mismatches 106;
                                                                                                                                                                                                                                                                                                                                  Length 399;
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PRIOR APPLICATION NUMBER: 09/189,527
PRIOR FILING DATE: 2001-01-04
PRIOR FILING DATE: 1998-11-10
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSEQ for Windows Version 4...
SEQ ID NO 11
SEQ ID NO 11
LENGTH: 283
TYPE: PRT
ORGANISM: homo sapiens
US-10-037-860-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 11, Application US/10037860
Publication No. US20020123114A1
GENERAL INFORMATION:
APPLICANT: Jerome B. Posner
APPLICANT: JOSEP O. Dalmau
APPLICANT: Myrna R. Rosenfeld
TITLE OF INVENTION: Ma FAMILY POLYPEPTIDES AND
TITLE OF INVENTION: ANTIBODIES
FILE REFERENCE: 2581.1004-004
CURRENT APPLICATION NUMBER: US/10/037,860
CURRENT APPLICATION 1004-01-04
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US-10-037-860-11
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Search completed: April 8,
Job time : 75.4975 secs
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Best Local Similarity
Matches 117; Conserv
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                                                                                           316 GPGPKPLSV
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                                                                                                                                                                                          122 KRWLAESLRGPALDLMHIVQADNPSISVEECLEAFKQVFGSLESRRTAQVRYLKTYQEEG
                                                                                                                                                                                                         139 EMLNYILDNVIQPLVESIWYKRLTLFSGKGHPRAWRGNFDPWLEHTNEVLEEWQVSDVEK 198
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                                                               246
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              2005, 13:35:12
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is derived by analysis of the total score distribution.

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Copyright (c) 1993 - 2005 Compus
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      BB
2 : US-08-318-837-9
4 US-09-949-016-10853
4 US-09-92-248-756A-15917
4 US-09-248-756A-15917
4 US-09-92-134-000C-5974
4 US-09-134-000C-5974
4 US-09-328-352-7656
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4 US-09-92-252-991A-31474
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3 US-08-9112-709-8
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3 US-09-941-244-8
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4 US-09-328-352-7783
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4, Appli
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17720, Appli
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US-09-189-527-13
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Sequence 13, Application US/09189527A
Patent No. 6387639
GENERAL INFORMATION:
APPLICANT: Jerome B. Posner
APPLICANT: Josep O. Dalmau
APPLICANT: Myrna R. Rosenfeld

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	US-09-189-527 Sequence 7, Patent No. ( Patent No. ( PAPLICANT: APPLICANT: APP	) 30 50 0 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2
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SLGRYRLLGKIFRKOEN 60	i-Ma Length 195;	Sequence 29636, A Sequence 323, App Sequence 10432, A Sequence 10724, A Sequence 10724, A Sequence 193, App Sequence 193, App	Sequence 31, Appl Sequence 52, Appl Sequence 52, Appl Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 1, Appli Sequence 6427, Ap Sequence 9445, Ap

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CURRENT APPLICATION NUMBER: US/09/189,527A
CURRENT FILING DATE: 198-11-10
NUMBER OF SEQ"ID NOS: 14
SOFTWARE: FABUSEQ for Windows Version 3.0
SEQ ID NO 4
LENGTH: 329
TYPE: PRT
ORGANISM: homo sapiens
US-09-189-527-4
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; TYPE: PRT
; ORGANISM: homo sapiens
US-09-189-527-13
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CURRENT FILING DATE: 1998-11-10
NUMBER OF SEQ ID NOS: 14
SOPTWARE: FASTSEQ for Windows-Version 3.0
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APPLICANT: Josep O. Dalmau
APPLICANT: Myrna R. Rosenfeld
TITLE OF INVENTION: Ma Family Polypeptides and Anti-Ma
TITLE OF INVENTION: Antibodies
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44.5%;...Score 443.5; DB 3;
Local Similarity 46.8%;..Pred. No. 8.2e-39;
hes 89; Conservative 34; Mismatches 64;
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181 EVWLEQATEIVKEW 194
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                                                                                                                                                       NAVLLELLEDTDVSAIPSEVQCKGGVWKVIFKTPNQDTEFLERLNLFLEKEGQTVSGMFR 121
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                                                     VLGFQ--NPTPTP--GPEMPAEMLNYILDNVIQPLVESIWYKRLTLFSGKGHPRAWRGNF
                                                                                         ALGQEALSPATVPCISPELLAHLLGQAMAHAPQPLL-PMRYRKLRVFSGSAVPAPEEESF 180
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RESULT 5
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Patent No. 598127
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CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/318,837
FILING DATE: 13-OCT-1994
CLASSIFICATION UMBER: PCT/EP 93/0102:
APPLICATION NUMBER: PCT/EP 93/0102:
APPLICATION NUMBER: PCT/EP 93/0102:
APPLICATION NUMBER: 92.401.231-3
PRIOR APPLICATION NUMBER: 92.401.231-3
APPLICATION NUMBER: 92.401.231-3
APPLICATION NUMBER: 92.401.231-3
APPLICATION NUMBER: 92.401.031-3
REFERENCE/DOCKET NUMBER: 19.683
REFERENCE/DOCKET NUMBER: 410.007
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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APPLICANT: FRANSE
APPLICANT: ANDRE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (212) 661-80
TELEFAX: (212) 661-8002
INFORMATION FOR SEQ ID NO:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
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ADDRESSEE: BIERMAN AND MUSERLIAN
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TITLE OF INVENTION:
TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                    y Match
8.8%; Score 87.5; DB
Local Similarity 27.1%; Pred. No. 0.55;
hes 45; Conservative 21; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH:
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                                                                                                                                  155 PLLPMRY------RKLRVFSGSAVPAPEEESFEVWLEQATEIVK 192
                                                                                                                                                                                                                    104 RINLFLEKEGQTVSGMFRALGQEALSPATVPCISPELLAHLLG------QAMAHAPQ 154
                                                                                                                                                                                                                                                                   109 KPFRDSSGANIYLEKTGELRLLV-RDIRGEPGQVQCFSLEQGGLF--VEATPQQDIS--R 163
                                                                                      220 QQVSVIYLRVNRLHRQKSRVFQ----PAPEDSGH--WLGHVTTLLQ 259
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Sequence 10853, Application US/09949016 Patent No. 6812339

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; SEQ ID NO 121
; LENGTH: 520
; TYPE: PRT
; ORGANIZSM: Candida albicans
US-09-792-024-121
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Best Local S
Matches 51
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PRIOR FILING DATE: 2000-10-20:
PRIOR PPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                APPLICANT: Bussey, Howard
TITLE OF INVENTION: Gens Disruption Methodologies for Drug
TITLE OF INVENTION: Targets Discovery
FILE REFERENCE: 10182-004-999:.
CURRENT APPLICATION NUMBER: US/09/792,024
CURRENT FILING DATE: 2001-02-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Roemer, Terry
APPLICANT: Jiang, Bo
APPLICANT: Boone, Charl
APPLICANT: Bussey, Howa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: VENTER, J. Craig et'al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ENGTH:
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o. 6783985
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20 LMVTGIPADFEEAEIQEVLOETLKSLGR------YRLLGKIFRKQENANAVLL 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3838
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                                                                                                                                                              Similarity
                                                                DYTTTRSVDLECS--ITGMIPPSSITRKIAEWVYANFSNVEEKSKRNVELELKFGKIIDK 298
                                                                                                 DWCRIMSVDEOKSLMVTG-IP-----ADFEEAEIQEVLQETLKSLGRYRLLGKIFRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---AQDTPARKTFEQALTGAFMSAVIKD 1041
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -VSGMFRALGQEALSPATVPCISPELLAHLLGQAMAH-----APQPLLPMRYRKLRVF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LCVDNLQPDFLYDHIQPVRAELMQALWRTLRNPADSISHVAYRVLGKF----GGSNRKML
                                                                                                                       8.5%; Score 84.5;
illarity 23.1%; Pred. No. 2.5
Conservative 39; Min-
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Charles
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24.0%; Pred. No. 22;
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; ORGANISM: Candida albicans
US-09-248-796A-15917
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US-09-248-796A-15917
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PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 15917
LENGTH: 527
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                                                                                                                                                                                                                                                                                                                                                          Matches
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICA:
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
                                                                                                                                                                                                                                                                                                                                                                             Match 8.5%;
Local Similarity 23.1%;
                                       153
                                                                                                                               113 GQTVSGM-----FRALGQEA-----LSPATVPCISPELLAHLLGQAMAHA 152
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                                                                                                                                                                                                                    58 QENANAVLLELLED --- TDVSAIPSEVQGKGGVWKVIFKTPNQDTEFLERLNLFLE--KE 112
                                                                                                                                                                                                                                                                                                                                                          51;
                                                                                                                                                                                                                                                                                                              7 DWCRIMSVDEQKSLMVTG-IP-----ADFEEAEIQEVLQETLKSLGRYRLLGKIFRK 57
                                                                                                                                                                                                                                                                  DYTTTRSVDLECS--ITGMIPPSSITRKIAEWVYANFSNVEEKSKRNVELELKFGKIIDK 305
PGSLF-----DLRLSMSLEIPVPQGNIESIITKNKPEMVRE
                                       POPILPMRYRKIRVFSGSAVPAPEEESFEVWLEQATEIVKE 193
                                                                                     GRKFKTLESDNTDSFYQLGRKGEHPKRIRVTKDNLLSPPRLVAIQKERVADL--
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                                                                                                                                                                                                                                                                                                                                                                                                    DB 4;
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US-09-902-540-13545

Sequence 13545, Application US/09902540

Patent No. 6833447

GEMERAL INFORMATION:

APPLICANT: Goldman, Barry S.

APPLICANT: Hinkle, Gregory J.

APPLICANT: Wisepand, Roger C.

APPLICANT: Wisepand, Roger C.

TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof

FILE REFERENCE: 38-10(15849)B

CURRENT FILING DATE: 2001-07-10

PRIOR APPLICATION NUMBER: 60/217,883

PRIOR APPLICATION NUMBER: 60/217,883

PRIOR FILING DATE: 2000-07-10

NUMBER OF SEQ ID NOS: 16825

SEQ ID NO 13545

LENGTH: 612

TYPE: PRT
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APPLICANT: Lynn Doucette-Stamm et al TITLE OF INVENTION: NUCLEIC ACID AND AMINO AC TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR FILE REFERENCE: 032796-032
CURRENT APPLICATION NUMBER: US/99/134,000C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/055,778
PRIOR APPLICATION NUMBER: US 60/055,778
PRIOR FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 6812
SOFTMARE: Patentin version 3.1
SEQ ID NO 5974
LENGTH: 547
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US-09-902-540-13545
                                                                                          US-09-248-796A-16474
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Patent No. 6617156
GENERAL INFORMATION:
APPLICANT: Keith Weinstock et
TITLE OF INVENTION: NUCLEIC AC
                                                      Sequence 16474, Application US/09248796A Patent No. 6747137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local S
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ORGANISM: Enterococcus faecalis
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                                                                                                                                                                                                    148 AMAHAPQPLLPMRYRKLRVF 167
                                                                                                                                                                                                                                                                                                              370 KLKNQNKSILIFQSKKNDHLMILQNLABRLQQALPITIRFALGNAYENLEDLPNSYIEAS 429
                                                                                                                                                                                                                                                                        30 EEAEIQEVLQE-----
                                                                                                                                                                                                                                                                                                                                              49 RLIGK-----IFRKQENANAVLLELLEDTDVSAIPSEVQ-GKGGVWKVIFKTPNQDTEFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                        44;
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22.0%; Pred. No. 4.
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   et al
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     AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 7656, Application US/09328352
Patent No. 6562958
GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BUNANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 16474
LENGTH: 285
                                                                                                                                                                                                                             Query Match 8.3
Best Local Similarity 25.3
Matches 36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS:
SEQ ID NO 7656
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Best Local Similarity
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CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-02-13
                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
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                                                                                                                                                                                                                                                                                                                            ORGANISM: Acinetobacter baumannii
                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
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364
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                                                                                                              76 AIPSEVQGKGGVWKVIFKTPNQDTEFLERLNLFLEKEGQTVSGM-----FRALGQE 126
                                                                                                                                                                                         30 EEAEIQEVLQETLKSLGR-------YRL-LGKIFRKQENANAVLLELLEDTDVS 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  74 VSAIPSEVQGKGGVWKVIFKTPNQD-----TEFLERLNLFL-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51,
  GSGKTTVGLLLMRLHQASGGQAL 386
                                                                          EIPERKRGLNGDEQIILEVKDLKKSFYSRKGLFGKEEFQAVKGVSFKLAKGKTLGLVGES 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -IW 266
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VNADPSKIAS----YQVFEDAAKADCAPSYALQFGSDLTTFVTQAEMYLMAPLLDQGYYV 145
                                    ALSPATVPCISPELLAHLLGQAM 149
                                                                                                                                                     EQGTAEQVLEQPKDVYTRALLYCRPQMSQRPYRLPVTSDFMRQE - - NNILVE - - QSFDVS
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25.2%; Pred. No. 6.1;
tive 22; Mismatches
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Pred. No. 2.1;
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RESULT 12 US-09-902-540-9777

Sequence 9777,

Application US/09902540

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APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
APPLICANT: Wiegand, Roger C.
FIILE OF INVENTION: Myxococcus xanthus Genome Sequences and User FILE REFERENCE: 38-10(15849))
CURRENT APPLICATION NUMBER: US/99/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/23/7,883
PRIOR APPLICATION NUMBER: 60/23/7,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 9777
LENGTH: 1442
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US-09-252-991A-31474
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                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 31474
LENGTH: 136
TYPE: DOT
                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 31474, Application US/09252991A
PAtent No. 6551795
GENERAL INFORMATION:
APPLICANT: MATC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patent No. 6833447
GENERAL INFORMATION:
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Best Local (
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                                                                   Matches
                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/252,991A CURRENT FILING DATE: 1999-02-18 PRIOR APPLICATION NUMBER: US 60/074,788 PRIOR FILING DATE: 1998-02-18:
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                                                                                   Local Similarity
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85
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   42 L-----KSLGRYRLLG--KIFRKQENANAVLLELLEDTDVSAIPSEV-----QGK 84
17 QKSLMVTGIP-----ADPEEAEIQEVLQETLKSLGRYRLLGKIFRKQENANAVLLELLED
                                                                   41;
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                                                                 Conservative
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                                                        8.1%; Score 80.5; DB 4;
21.6%; Pred. No. 0.92;
tive 24; Mismatches 48;
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                                                                                                           Length 136;
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Matches
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                                                                                                                                                  Query Match
Best Local
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                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 7-MAY-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/016,774
FILING DATE: 7-MAY-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OFERATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Force, Thomas
APPLICANT: Kyriakis, John M.
APPLICANT: Pombo, Celia M.
                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: 617/542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Bonventre, Joseph
TITLE OF INVENTION: SOK-1 AND METHODS OF USE
NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                     MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                           NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34.
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/852,743 FILING DATE: 7-MAY-1997
                                                                                                                                                                                                                                   TOPOLOGY:
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                              57 KQENANAVLLELLEDTDVSAIPSEVQGKGGVWKVIFKTPNQDTEFLERLNLFLEKEGQTV 116
                                                                  73 LWIVMEYCGAGSVSDIIRLRNKTL-----TEDEIATILQSTLKGLEYLHFMRKIHR 123
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                                                                                               2 LALLEDWCRIMSVDE-----OKSLMVTGIPADFEEAEIQEVLQETLKSLGRYRLLGKIFR 56
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                                                                                                                                                                                                                                                 : 270 amino acids
amino acid
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                                                                                                                                                                                                                                                                                                                                            617/542-8906
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                                                                                                                                     Conservative
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                                                                                                                                                  8.1%;
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                                                                                                                                                                                                                                                                                                        5
                                                                                                                                     26;
                                                                                                                                 Score 80.5; DE Pred. No. 2.5; 26; Mismatches
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-NTEGHAKLADFGVAGQLTDTMAKRN-----TV 159
                                                                                                                                                                    DB 2;
                                                                                                                                     85;
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                                                                                                                                                                  Length 270;
                                                                                                                                     Indels 45;
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US-09-185-370-5
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                                                                                                                                                                                                                                                                                                                                                                                                                               TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Force, Thomas
APPLICANT: Kyriakis, John M.
APPLICANT: Pombo, Celia M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/852,743
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/185,370
FILING DATE:
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ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Fraser, Janis K. REGISTRATION NUMBER: 34. REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
TOPOLOGY: linear
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TLE OF INVENTION: SOK-1 AND METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH:
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174 APEEESFEVWLEQATEIVKE 193
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                                                                                                                         124 DIKAGNILL-----
                                                                                                                                                     57 KQENANAVILELLEDTDVSAIPSEVQGKGGVWKVIFKTFNQDTEFLERLNLFLEKEGQTV 116
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                                                                                      SGMFRALGQEALSPATVPCISPELLAHLLGQAMAHAPQP---LLPMRYRKLRVFSGSAVP 173
                                                                                                                                                                                       LWIVMEYCGAGSVSDIIRLRNKTL-----TEDEIATILQSTLKGLEYLHFMRKIHR 123
                                                                                                                                                                                                                                                                                                                                                                                                             270 amino acids ::
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216 PPTFRKPELWSDNFTDFVKQ 235

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Search completed: April 8, 2005, 12:52:55 Job time: 16.9789 secs

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Minimum DB
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No.
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Maximum Match 100%
Listing first 45-summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Scoring table:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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seq length: 2000000000
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996
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1486.133 Million cell updates/sec
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1: /cgn2_6/ptodata/1/pubpaa/USO:
1: /cgn2_6/ptodata/1/pubpaa/PCT
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Copyright (c) 1953 - 2005 Compugen Ltd
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n2 6/ptcdata/1/pubpaa/US10B PUBCOMB.pep: *
n2 6/ptcdata/1/pubpaa/US10C PUBCOMB.pep: *
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n2 6/ptcdata/1/pubpaa/US10D PUBCOMB.pep: *
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13: US-10-037-860-4
10: US-09-804-014A-40
10: US-09-804-014A-73
10: US-09-804-014A-74
10: 'US-09-804-014A-74
10: 'US-09-804-014A-74
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                                                                                                                                      Sequence 7, Appli
Sequence 42, Appl
Sequence 11, Appli
Sequence 7, Appli
Sequence 7, Appli
Sequence 13, Appli
Sequence 4, Appli
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                    Sequence 39,
Sequence 1, A
                                                                 Sequence 40, Appl
Sequence 73, Appl
Sequence 74, Appl
Sequence 16,
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43.8 45: 15 US-10-341-434-10  \$42.16 US-10-094-749-1978 Sequence 21  34.6 399 15 US-10-094-749-1978 Sequence 19  32.9 204 14 US-10-092-386-33747 Sequence 33  30.7 1200 10 US-09-804-761-34645 Sequence 34  27.1 116 9 US-09-804-761-34645 Sequence 34  27.1 116 9 US-09-804-765A-2992 Sequence 34  14.7 538 16 US-10-291-178-355 Sequence 35  13.8 584 15 US-10-291-178-355 Sequence 35  13.8 15 US-10-291-178-355 Sequence 36  10.0 403 15 US-10-094-466-38 Sequence 36  10.0 403 15 US-10-094-466-38 Sequence 36  10.0 403 15 US-10-095-159-26 Sequence 36  10.0 403 15 US-10-095-129-213 Sequence 27  10.0 403 15 US-10-097-72-100-1 Sequence 27  10.0 403 15 US-10-097-72-100-1 Sequence 27  10.0 403 15 US-10-369-493-443 Sequence 17  10.0 403 15 US-10-369-493-720 Sequence 37  10.0 403 15 US-10-369-493-720 Sequence 37  10.0 403 15 US-10-369-493-720 Sequence 27  10.0 403 15 US-10-09-13-678-2 Sequence 27  10.0 403 15 US-10-09-13-678-2 Sequence 27  10.0 403 15 US-10-09-1458-3 Sequence 28  10.0 404 15 US-10-09-1458-3 Sequence 29  10.0 403 15 US-10-09-1458-3 Sequence 29  10.0 403 15 US-10-09-1458-3 Sequence 29  10.0 403 15 US-10-09-1458-3 Sequence 20  10.0 403 15 US-10-10425-114-55513 Sequence 20	equence 19955	US-10-437-963-1995		•	82	4 5
43.8 351 15 US-10-341-434-10  \$43.6 452 16 US-10-408-765A-238 Sequence 21  34.6 399 15 US-10-094-749-1978 Sequence 19  32.9 204 14 US-10-029-386-3747 Sequence 33  30.7 120 10 US-09-864-761-34645 Sequence 34  27.1 116 9 US-09-864-765A-2992 Sequence 34  27.1 116 9 US-10-291-172-355 Sequence 29  13.8 584 15 US-10-221-279-355 Sequence 35  13.8 584 15 US-10-221-279-355 Sequence 36  9.8 402 17 US-10-99-436-38 Sequence 36  9.8 402 17 US-10-295-1515-1208 Sequence 20  8.9 342 13 US-10-001-887-201 Sequence 20  8.9 342 13 US-10-001-887-201 Sequence 21  8.8 1357 15 US-10-295-077-1199 Sequence 21  8.8 1357 15 US-10-295-077-1199 Sequence 21  8.8 1357 15 US-10-295-077-1199 Sequence 21  8.8 1357 15 US-10-369-433-730 Sequence 21  8.6 1083 15 US-10-369-433-730 Sequence 21  8.7 15 US-10-369-433-730 Sequence 21  8.8 16 1083 15 US-10-369-433-730 Sequence 21  8.9 16 US-10-032-585-7035 Sequence 27  8.4 1638 13 US-10-090-458-5 Sequence 27  8.4 1642 13 US-10-090-458-5 Sequence 27  8.4 1642 13 US-10-156-763-7 Sequence 27  8.4 1642 13 US-10-156-763-7 Sequence 27  8.4 1642 14 US-10-091-458-5 Sequence 5  8.4 3613 14 US-10-156-763-7 Sequence 5  8.4 3613 14 US-10-156-763-7 Sequence 27  8.5 Sequence 27  8.6 361 14 US-10-156-763-7 Sequence 27  8.7 Sequence 27  8.8 Sequence 27  8.9 Sequence 27	e 55513,	US-10-425-114-5551		•	82	44
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43.8 351 15 US-10-341-434-10  \$43.6 43.5 16 US-10-408-765A-238  \$4.6 399 15 US-10-094-749-1978  \$4.6 399 15 US-10-094-749-1978  \$4.6 399 15 US-10-094-749-1978  \$4.6 399 15 US-10-094-749-1978  \$4.6 399 15 US-10-029-386-3747  \$5.6 204 14 US-09-804-01.4A-41  \$5.6 204 15 US-10-291-172-355  \$5.6 204 15 US-10-094-466-38  \$5.6 205 17 US-10-094-466-38  \$5.6 205 17 US-10-095-151-208  \$5.6 205 17 US-10-091-857-201  \$5.6 205 13 US-10-087-192-213  \$5.6 205 13 US-10-087-192-213  \$5.6 205 14 US-10-295-27-1199  \$5.6 205 16 US-10-295-27-1199  \$5.6 205 16 US-10-369-493-735  \$5.6 205 14 US-10-369-493-793  \$5.7 205 14 US-10-369-493	10	US-10-156-761-1043		•	84	42
43.8 351 15 US-10-341-434-10  43.6 452 16 US-10-408-765A-238  34.6 399 15 US-10-094-719-1978  32.9 204 14 US-10-029-386-3747  32.9 204 14 US-00-29-386-3747  30.7 120 10 US-09-864-761-34645  27.1 116 9 US-09-864-761-34645  27.1 116 9 US-09-864-765A-2992  584 15 US-10-291-172-355  584 15 US-10-221-2778-355  584 15 US-10-221-278-355  584 15 US-10-221-278-355  584 15 US-10-291-172-355  584 15 US-10-291-172-173  8.8 317 15 US-10-291-173-18  8.9 342 13 US-10-001-887-201  8.8 313 13 US-10-291-173-193  584 15 US-10-291-193-193  584 15 US-10-349-493-720  8.6 1083 15 US-10-369-493-730  8.6 1083 15 US-10-369-493-730  8.7 350 9 US-09-731-7903  585 20 14 US-10-32-585-7035  585 20 14 US-10-090-458-5	e 5,	US-10-005-338E		•	84	41
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43.8 351 15 US-10-341-434-10  Sequence 21  34.6 399 15 US-10-094-749-1978 Sequence 19  34.6 399 15 US-10-094-749-1978 Sequence 19  32.9 204 14 US-10-029-386-33747 Sequence 31  30.7 120 10 US-09-804-761-34645 Sequence 31  27.1 116 9 US-09-864-7761-34645 Sequence 32  14.7 538 16 US-10-291-172-355 Sequence 32  13.8 584 15 US-10-291-172-355 Sequence 32  13.8 584 15 US-10-094-466-38 Sequence 35  10.0 403 15 US-10-094-466-38 Sequence 36  9.8 402 17 US-10-959-539-26 Sequence 36  9.8 402 17 US-10-096-115-1208 Sequence 26  8.9 337 15 US-10-001-857-201 Sequence 10  8.8 1357 15 US-10-097-77-100-1  8.8 1357 15 US-10-295-727-1199 Sequence 11  8.8 1357 15 US-10-295-03-3443 Sequence 27  8.6 1083 15 US-10-295-493-7493  8.6 1084 15 US-10-286-128-4991 Sequence 49  8.6 1084 15 US-10-286-128-4991 Sequence 27  8.6 1084 15 US-10-369-493-7790 Sequence 27  8.5 520 14 US-10-369-433-17903 Sequence 27  8.6 1083 15 US-10-369-433-17903 Sequence 27  8.7 Sequence 27  8.8 520 14 US-10-032-865-7035 Sequence 27  8.9 Sequence 27  8.10 Sequence 27  8.11 Sequence 27  8.12 Sequence 27  8.12 Sequence 27  8.12 Sequence 27  8.13 Sequence 27  8.14 336 9 US-09-745-763-17	e 2,	US-10-090-45		•	84	9
43.8 351 15 US-10-341-434-10 Sequence 20 43.6 439 15 US-10-094-749-1978 Sequence 19 34.6 399 15 US-10-094-749-1978 Sequence 19 32.9 204 14 US-10-029-386-3747 Sequence 33 30.7 210 10 US-09-864-761-34645 Sequence 34 27.1 116 9 US-09-864-761-34645 Sequence 26 14.7 538 16 US-10-291-78-355 Sequence 27 13.8 584 15 US-10-221-278-355 Sequence 35 13.8 584 15 US-10-221-278-355 Sequence 36 9.8 402 17 US-10-94-466-38 Sequence 36 9.8 402 17 US-10-959-539-26 Sequence 26 9.8 337 15 US-10-091-857-201 Sequence 27 8.8 255 13 US-10-001-857-201 Sequence 27 8.8 315 10 US-09-727-1109 Sequence 27 8.8 315 10 US-09-727-119 Sequence 27 8.8 315 US-10-395-433-443 Sequence 37 8.6 1083 15 US-10-369-433-720 Sequence 24 8.6 1083 15 US-10-369-433-720 Sequence 49 8.6 1083 15 US-10-369-433-720 Sequence 49 8.6 1084 15 US-10-369-433-720 Sequence 27 8.5 520 14 US-10-32-585-7035 Sequence 70	equence 17, A	US-09-745-763		•	84	38
43.8 351 15 US-10-341-434-10  43.6 352 16 US-10-408-765A-2385 Sequence 10,  43.6 359 15 US-10-094-749-1978 Sequence 2385  34.6 359 15 US-10-094-749-1978 Sequence 2385  32.9 204 14 US-10-029-386-33747 Sequence 374  30.7 120 10 US-09-804-014A-41 Sequence 3464  27.1 116 9 US-09-864-761-34645 Sequence 3464  27.1 116 9 US-09-864-761-34645 Sequence 3464  13.8 584 15 US-10-221-2792 Sequence 355,  13.8 584 15 US-10-221-279-355 Sequence 35,  13.8 584 15 US-10-094-466-38 Sequence 36,  9.8 402 17 US-10-99-539-26 Sequence 20,  8.9 337 15 US-10-296-115-1208 Sequence 20,  8.8 311 10 US-10-296-115-1208 Sequence 21,  8.8 311 10 US-10-296-115-1208 Sequence 21,  8.8 311 10 US-10-397-192-213 Sequence 21,  8.8 315 11 US-10-295-027-1199 Sequence 1199  8.8 1357 15 US-10-369-433-443 Sequence 354,  8.6 1083 15 US-10-369-433-7202 Sequence 7202  8.6 1083 15 US-10-389-493-7203 Sequence 7203  8.6 1083 15 US-10-389-493-7303 Sequence 7203  8.7 Sequence 7203  8.8 US-10-389-493-7303 Sequence 7203  8.9 Sequence 204,  8.9 Sequence 205,  8.9 Sequence 206,  8.9 Sequence 206,  8.9 Sequence 206,  8.9 Sequence 207,  8.9 Sequence 207,  8.9 Sequence 208,  8.9 Sequence 207,  8.9 Sequence 208,  8.9 Sequence 208,  8.9 Sequence 209,  8	7035	US-10-032-585-7		•	•	37
43.8 351 15 US-10-341-434-10 Sequence 20 43.6 452 16 US-10-094-749-1978 Sequence 21 34.6 399 15 US-10-094-749-1978 Sequence 19 32.9 204 14 US-10-029-386-33747 Sequence 33 30.7 120 10 US-09-804-014A-41 Sequence 31 27.1 116 9 US-09-804-75A-2992 Sequence 32 13.8 584 15 US-10-291-172-355 Sequence 32 13.8 584 15 US-10-291-172-355 Sequence 35 13.8 584 15 US-10-094-466-38 Sequence 35 10.0 403 15 US-10-094-466-38 Sequence 36 9.8 402 17 US-10-959-539-26 Sequence 26 9.8 402 17 US-10-095-115-1208 Sequence 26 9.3 337 15 US-10-091-15-1208 Sequence 27 8.8 3859 16 US-09-727-100-1 Sequence 21 8.8 3859 16 US-10-408-765A-354 Sequence 35 8.6 1083 15 US-10-369-493-443 Sequence 35 8.6 1084 15 US-10-369-493-793 Sequence 44 8.6 1083 15 US-10-369-493-793 Sequence 49 8.6 1084 15 US-10-369-493-793 Sequence 79 8.6 1084 15 US-10-369-493-793 Sequence 79 8.6 1084 15 US-10-369-493-793 Sequence 79	equence 2, Ap	US-09-213-678-		•	84.5	36
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43.8 351 15 US-10-341-434-10  43.6 452 16 US-10-408-765A-238 Sequence 21  34.6 399 15 US-10-094-749-1978 Sequence 13  32.9 204 14 US-10-029-386-33747 Sequence 33  30.7 120 10 US-09-864-761-34645 Sequence 37  27.1 116 9 US-09-864-761-34645 Sequence 37  13.8 584 15 US-10-408-765A-2992 Sequence 35  13.8 584 15 US-10-291-172-355 Sequence 35  13.8 584 15 US-10-291-172-355 Sequence 35  13.8 584 15 US-10-291-172-355 Sequence 35  13.8 584 15 US-10-094-466-38 Sequence 36  9.8 402 17 US-10-959-539-26 Sequence 26  9.3 337 15 US-10-094-155-1208 Sequence 26  9.3 337 15 US-10-097-152-21 Sequence 27  8.8 385 15 US-10-072-7100-1  8.8 311 10 US-09-727-100-1  8.8 385 16 US-10-408-765A-354 Sequence 35  8.6 1083 15 US-10-369-493-4443 Sequence 44	equence 7202,	US-10-369-493-		•	96	ü
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43.8 351 15 US-10-341-434-10  43.6 452 16 US-10-408-765A-2385 Sequence 23  34.6 399 15 US-10-094-749-1978 Sequence 23  32.9 204 14 US-10-029-386-33747 Sequence 33  37.7 1120 10 US-09-804-014A-41 Sequence 34  27.7 116 9 US-09-804-761-34645 Sequence 346  14.7 538 16 US-10-408-765A-2992 Sequence 34  13.8 584 15 US-10-291-172-355 Sequence 35  13.8 584 15 US-10-291-278-355 Sequence 35  10.0 403 15 US-10-094-466-38 Sequence 36  9.8 402 17 US-10-94-66-38 Sequence 36  9.8 337 15 US-10-296-115-1208 Sequence 26  9.3 337 15 US-10-094-266-38 Sequence 27  8.8 255 13 US-10-087-192-213 Sequence 21, Sequ	equence 11	US-10-295-027-		•	7.	30
43.8 351 15 US-10-341-434-10 Sequence 20 43.6 452 16 US-10-408-765A-238 Sequence 21 34.6 399 15 US-10-094-749-1978 Sequence 19 32.9 204 14 US-10-029-386-33747 Sequence 33 30.7 120 10 US-09-804-014A-41 Sequence 31 27.1 116 9 US-09-864-761-34645 Sequence 22 13.8 584 15 US-10-291-172-355 Sequence 35 13.8 584 15 US-10-291-172-355 Sequence 35 13.8 584 15 US-10-291-172-355 Sequence 35 10.0 403 15 US-10-094-466-38 Sequence 36 9.8 402 17 US-10-959-539-26 Sequence 26 9.3 337 15 US-10-094-365-38 Sequence 26 9.3 337 15 US-10-094-365-38 Sequence 26 9.3 337 15 US-10-094-365-39 Sequence 26	equence 1,	US-09-727-100-		•		29
43.8 351 15 US-10-341-434-10 43.6 452 16 US-10-408-765A-2385 Sequence 21 34.6 399 15 US-10-094-749-1978 Sequence 19 32.9 204 14 US-10-029-386-33747. Sequence 33 30.7 120 10 US-09-804-014A-41 Sequence 41 27.1 116 9 US-09-864-761-34645 Sequence 29 14.7 538 16 US-10-408-765A-2992 Sequence 29 13.8 584 15 US-10-221-172-355 Sequence 35 13.8 584 15 US-10-221-278-355 Sequence 35 13.8 584 15 US-10-221-278-355 Sequence 35 13.8 584 15 US-10-221-278-355 Sequence 36 9.8 402 17 US-10-94-466-38 Sequence 38 9.8 402 17 US-10-296-1155-1208 Sequence 29 8.9 342 13 US-10-001-887-201 Sequence 20	e 21	US-10-087-192	-	•	87.5	28
43.8 351 15 US-10-341-434-10  43.6 452 16 US-10-408-765A-2385 Sequence 23  34.6 399 15 US-10-094-749-1978 Sequence 23  32.9 204 14 US-10-029-386-33747 Sequence 33  30.7 120 10 US-09-804-014A-41 Sequence 34  27.1 116 9 US-09-864-761-34645 Sequence 346  14.7 538 16 US-10-408-765A-2992 Sequence 35  13.8 584 15 US-10-291-172-355 Sequence 35  13.8 584 15 US-10-221-278-355 Sequence 35  10.0 40.3 15 US-10-294-466-38 Sequence 36  9.8 402 17 US-10-959-539-26 Sequence 26  9.3 337 15 US-10-296-115-1208 Sequence 26	20	US-10-001-857	_	•		27
43.8 351 15 US-10-341-434-10  43.6 452 16 US-10-408-765A-238 Sequence 23  34.6 399 15 US-10-094-749-1978 Sequence 23  32.9 204 14 US-10-029-386-33747 Sequence 33  30.7 120 10 US-09-804-014A-41 Sequence 31  27.1 116 9 US-09-864-761-34645 Sequence 29  13.8 584 15 US-10-408-765A-2992 Sequence 35  13.8 584 15 US-10-291-172-355 Sequence 35  13.8 584 15 US-10-291-278-355 Sequence 35  10.0 403 15 US-10-094-466-38 Sequence 36  9.8 402 17 US-10-959-539-26 Sequence 26	12	US-10-296-115-120		•	ν.	26
43.8 351 15 US-10-341-434-10 43.6 452 16 US-10-408-765A-2385 Sequence 21 34.6 399 15 US-10-094-749-1978 Sequence 19 32.9 204 14 US-10-029-386-33747. Sequence 33 30.7 120 10 US-09-804-014A-41 Sequence 34 27.1 116 9 US-09-864-761-34645 Sequence 29 14.7 538 16 US-10-408-765A-2992 Sequence 29 13.8 584 15 US-10-221-278-355 Sequence 35 13.8 584 15 US-10-221-278-355 Sequence 35 10.0 403 15 US-10-094-466-38 Sequence 38	26	US-10-959-539-	_	•	7.	25
43.8 351 15 US-10-341-434-10  43.6 452 16 US-10-408-765A-299  13.6 399 15 US-10-094-749-1978 Sequence 23: 32.9 204 14 US-10-029-386-33747; Sequence 33: 30.7 120 10 US-09-804-014A-41 Sequence 41: 27.1 116 9 US-09-804-761-34645 Sequence 346: 14.7 538 16 US-10-408-765A-2992 Sequence 23: 13.8 584 15 US-10-221-278-355 Sequence 35:	38	· US-10-094-466	_	•	٠	24
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43.8 351 15 US-10-341-434-10 43.6 452 16 US-10-408-765A-2385 Sequence 23 34.6 399 15 US-10-094-749-1978 Sequence 19 32.9 204 14 US-10-029-386-33747. Sequence 33 30.7 120 10 US-09-804-014A-41 Sequence 41 27.1 116 9 US-09-864-761-34645 Sequence 29 14.7 538 16 US-10-408-765A-2992 Sequence 29	35	US-10-291-172-35	-	w	1.3	22
43.8 351 15 US-10-341-434-10 43.6 452 16 US-10-408-765A-2385 Sequence 21 34.6 399 15 US-10-094-749-1978 Sequence 19 34.6 399 15 US-10-098-386-33747. Sequence 33 30.7 120 10 US-09-804-014A-41 Sequence 31 27.1 116 9 US-09-864-761-34645 Sequence 346	e 29	US-10-408-765A-299		4	146	21
43.8 351 15 US-10-341-434-10 Sequence 10, Ap 43.6 452 16 US-10-408-765A-2385 Sequence 2385, 34.6 399 15 US-10-094-749-1978 Sequence 1978, 32.9 204 14 US-10-029-386-33747, 30.7 120 10 US-09-804-014A-41 Sequence 41, Ap	346	US-09-864-761-3464		7	270	20
43.8 351 15 US-10-341-434-10 43.6 452 16 US-10-408-765A-2385 Sequence 2385, 34.6 399 15 US-10-094-749-1978 Sequence 1978, 32.9 204 14 US-10-029-386-33747. Sequence 33747,	e 41, App	US-09-804-014A-4	Ī		306	19
43.8 351 15 US-10-341-434-10 Sequence 10, Ap 43.6 452 16 US-10-408-765A-2385 Sequence 2385, 34.6 399 15 US-10-094-749-1978 Sequence 1978,	equence 33747,	US-10-029-386-3374			327.5	18
43.8 351 15 US-10-341-434-10 Sequence 10, Ap 43.6 452 16 US-10-408-765A-2385 Sequence 2385,	equence 1978,	US-10-094-749-197		4.	345	17
43.8 351 15 US-10-341-434-10 Sequence 10, App	equence 2385,	US-10-408-765A-238		ω.	ω	16
	equence 10, App	US-10-341-434		ü	436	15
43.8 351 10 US-09-969-680A-1 Sequence 1, Appl	equence 1, Appl	US-09-969-680A-		•	436	14

## **ALIGNMENTS**

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; TYPE: PRT
; ORGANISM: homo sapiens
US-10-037-860-7
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7
                                                                                                                                                                                                  Query Match 100.0%; Score 996; DB 13; Best Local Similarity 100.0%; Pred. No. 4.2e-92; Matches 195; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 7, Application US/10037860 Publication No. US20020123114A1
                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: MA FAMILY POLYPEPTIDES
TITLE OF INVENTION: MATHBODIES
FILE REFERENCE: 2581.1004-004
CURRENT APPLICATION NUMBER: US/10/037,860
CURRENT FILING DATE: 2001-01-04
PRIOR APPLICATION NUMBER: 09/189,527
PRIOR FILING DATE: 1998-11-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Jerome B. Posner
APPLICANT: Josep O. Dalmau
APPLICANT: Myrna R. Rosenfeld
121 RALGQEALSPATVPCISPELLAHLLGQAMAHAPQPLLPMRYRKLRVFSGSAVPAPEEESF 180
                                                           61 ANAVILELLEDTDVSAIPSEVOGKGGVWKVIFKTPNODTEFLERLNLFLEKEGGTVSGMF 120
                                                                                                                     1 PLALLEDWCRIMSVDEQKSLMVTGIPADFEEAEIQEVLQETLKSLGRYRLLGKIFRKQEN
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                                            120
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Sequence 11, Application US/10037860
Publication No. US20020123114A1.
GENERAL INFORMATION:
APPLICANT: Jerome B. Posner
APPLICANT: JOSEP O. Dalmau
APPLICANT: Myrna R. Rosenfeld,
TITLE OF INVENTION: MA FAMILY POLYPEPTIDES AND TITLE OF INVENTION NUMBER: US/10/037,860
CURRENT APPLICATION NUMBER: US/10/037,860
CURRENT FILING DATE: 2001-01-04
PRIOR APPLICATION NUMBER: 09/189,527
PRIOR FILING DATE: 1998-11-10
NUMBER OF SEQ ID NOS: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoding Same
FILE REFERENCE: 15966-721 US
CURRENT APPLICATION NUMBER: US/09/804,014A
CURRENT FILING DATE: 2002-04-24
PRIOR APPLICATION NUMBER: 60/188,316
PRIOR APPLICATION NUMBER: 60/188,277
PRIOR APPLICATION NUMBER: 60/188,277
PRIOR APPLICATION NUMBER: 60/18,277
PRIOR FILING DATE: 2000-03-10
PRIOR FILING DATE: 2000-03-10
PRIOR PILING DATE: 2000-03-10
PRIOR PILING DATE: 2000-03-10
PRIOR APPLICATION NUMBER: 60/189,139
PRIOR APPLICATION NUMBER: 60/189,140
PRIOR APPLICATION NUMBER: 60/199,401
PRIOR APPLICATION NUMBER: 60/199,401
PRIOR APPLICATION NUMBER: 60/199,401
PRIOR APPLICATION NUMBER: 60/190,401
PRIOR PILING DATE: 2000-03-17
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US-10-037-860-11
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US-09-804-014A-42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 120; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 60.6%: Score 604; DB 10; Best Local Similarity 100.0%; Pred. No. 7.5e-53;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 42, Application US/09804014A Publication No. US20030064489A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Vernet, Corine
APPLICANT: Fernandes, Elma
APPLICANT: Shimkets, Richard
APPLICANT: Spaderna, Steven
APPLICANT: Majumder, Kumud
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PRIOR FILING DATE: 2000-03-17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Li, Li
APPLICANT: Padigaru,
APPLICANT: Vernet, Co
APPLICANT: Fernandes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 120
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APPLICANT: BAUGHN, Mariah R.

APPLICANT: LU, Dyung Aina M.

APPLICANT: PATTERSON, Chandra

FILE REFERSON, CHANDRE ASSOCIATED PROTEINS

FILE REFERENCE: PF-0731 USA

CURRENT APPLICATION NUMBER: US/09/965,529

CURRENT FILING DATE: 2001-09-26

PRIOR APPLICATION NUMBER: 60/149,641; 60/164,203; PCT/US00/22315

PRIOR FILING DATE: 1999-08-17; 1999-11-09; 2000-08-14

NUMBER OF SEQ ID NOS: 74

SOFTWARE: PERL Program

SEQ ID NO 7-

I LENDER: 1000-08-17
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APPLICANT: LAL, Preeti
APPLICANT: YUE, Henry
APPLICANT: TANG, Y. Tom
APPLICANT: BANDMAN, Olga
APPLICANT: BURFORD, Neil
APPLICANT: AZIMZAI, Yaida
APPLICANT: BUGHON, Mariah R
APPLICANT: BUGHON, Mariah R
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US-09-965-529-7
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                                                                                                                                                                                                                                                                                                                      Query Match 46.8%;
Best Local Similarity 47.9%;
Matches 93; Conservative 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 7, Application US/0996529 Publication No. US20020182671A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 113;
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TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 353
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. US20020182671A1 2483172CD1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
178 DPWLEHTNEVLEEW 191
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                                                                                                                     122 ALGQEALSPATVPCISPELLAHLLGQAMAHAPQPLL-PMRYRKLRVFSGSAVPAPEEESF 180
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                                                                                                                                                                                                                                                                           2 LALLEDWCRIMSVDEQKSLMVTGIPADFEEAEIQEVLQETLKSLGRYRLLGKIFRKQENA 61
                                                                                                                                                            VLGFQ--NPTPTP--GPEMPAEMLNYILDNVIQPLVESIWYKRLTLFSGRDIPGPGEETF 177
                                    EVWLEQATEIVKEW 194
                                                                                                                                                                                                                                         MTLLEDWCRGMDVNSQRALLVWGIPVNCDEAEIEETLQAAMPQVS-YRMLGRMFWRBENA 61
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                                                                                                                                                                                                                                                                                                                        ; Score 466; DB 9;
; Pred. No. 2.9e-38;
38; Mismatches 57
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Pred. No. 3.3e-51;
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RESULT 5

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APPLICANT: TANG, Y. Tom; BANDMAN, Olga
APPLICANT: BURFORD, Neil; AZIMZAL, Yalda
APPLICANT: BURFORD, Neil; AZIMZAL, Yalda
APPLICANT: BAUGHN, Mariah R.; IU, Dyung Aina M.
APPLICANT: PATTERSON, Chandra
TITLE OF INVENTION: MEMBRANE ASSOCIATED PROTEINS
FILE REFERENCE: PF-0731-1 USA
CURRENT APPLICATION NUMBER: US/09/969,680A
CURRENT FILING DATE: 2001-10-02
PRIOR APPLICATION NUMBER: US/09/2315
PRIOR APPLICATION NUMBER: 60/149,641
                                                                                                                                                           APPLICANT: Jerome B. Posner
APPLICANT: JOSEP O. Dalmau
APPLICANT: MYDNAR R. ROSENFEID
TITLE OF INVENTION: MA FAMILY POLYPEPTIDES AN
TITLE OF INVENTION: MATHRODIES
FILE REFERENCE: 2581.1004-004
CURRENT APPLICATION NUMBER: U$/10/037,860
CURRENT FILING DATE: 2001-01-04
PRIOR APPLICATION NUMBER: 09/189,527
PRIOR FILING DATE: 1998-11-10
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PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 74
SOFTWARE: PERL Program
SEQ ID NO 7
                                                                                             NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
SEQ ID NO 13
                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION
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TYPE: PRT
ORGANISM: homo sapiens
-10-037-860-13
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TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. US20030124649A1 2483172CD1
                                                                          LENGTH: 463
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                                                                                                                     for Windows Wersion
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Publication No. US20020123114A1
GENERAL INFORMATION:
APPLICANT: Jerome B. Posner
APPLICANT: Josep O. Dalmau
APPLICANT: Myrna R. Rosenfeld
TITLE OF INVENTION: Ma FAMILY POLYPEPTIDES AND ANTI-MA
TITLE OF INVENTION: ANTIBODIES
ETIT BEFERENCE: JEST 100.000
                                                                                                                                                                                                                                                                                                       Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 4
LENGTH: 329
TYPE: PRT
ORGANISM: homo sapiens
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: 2581.1004-004
CURRENT APPLICATION NUMBER: US/10/037,860
CURRENT FILING DATE: 2001-01-04
PRIOR APPLICATION NUMBER: 09/189,527
PRIOR FILING DATE: 1998-11-10
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FASTSEQ for Windows Version 4.0
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178 DPWLEHTNEVLEEW
                                   181 EVWLEQATEIVKEW 194
                                                                         122 VLGFQ--NPTPTP--GPEMPAEMLNYILDNVIOPLVESIWYKRLTLFSGKGHPRAWRGNF
                                                                                                           122 ALGQEALSPATVPCISPELLAHLLGQAMAHAPQPLL-PMRYRKLRVFSGSAVPAPEEESF 180
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                                                                                                                                                                         62 NAVLLELLEDTDVSAIPSEVQGKGGVWKVIFKTPNQDTEFLERLNLFLEKEGQTVSGMFR 121
                                                                                                                                                   62 KAALLELTGAVDYAAIPREMPGKGGVWKVLFKPPTSDAEFLERLHLFLAREGWTVQDVAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62 AQAILLELAQDIDYALLPREIPGKGGPWEVIVKPRNSDGEFLNRLNRFLEEERRTVSDMN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 ANAVLLELLEDTDVSAIPSEVQGKGGVWKVIFKTPNQDTEFLERLNLFLEKEGQTVSGMF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93;
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                                                                                                                                                                                                                                                                                                         90;
                                                                                                                                                                                                                                                                 2 LALLEDWCRIMSVDEQKSLMVTGIPADFEEAEIQEVLQETLKSLGRYRLLGKIFRKQENA
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nilarity 47.7%;
Conservative 3
                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                       44.3%; Score 441; DB 13;
46.4%; Pred. No. 8.9e-36;
tive 37; Mismatches 61;
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Pred. No. 9.7e-38;
4; Mismatches 65;
                                                                                                                                                                                                                                                                                                       61;
                                                                                                                                                                                                                                                                                                                                           Length 329;
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US-09-804-014A-40

Sequence 40, Application US/09804014A publication No. US20030064489A1 GENERAL INFORMATION:
APPLICANT: Li, Li
APPLICANT: Padigaru, Muralidhara

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Best Local (
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APPLICANT:
APPLICANT: Spaderna, Steven: APPLICANT: Majumder, Kumud V;
APPLICANT: Majumder, Kumud V;
TITLE OF INVENTION: NOVel Polypeptides and Nucleic Acids Encoding Same
FILE REFERENCE: 15966-721 US
CURRENT APPLICATION NUMBER: 40/09/804,014A
CURRENT FILING DATE: 2002-04:34
PRIOR APPLICATION NUMBER: 60/188,316
PRIOR FILING DATE: 2000-03-10:
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PRIOR FILING DATE: 2000-03-14:
PRIOR APPLICATION NUMBER: 60/189,140
PRIOR FILING DATE: 2000-03-14
PRIOR APPLICATION NUMBER: 60/190,401
PRIOR FILING DATE: 2000-03-17
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NUMBER OF SEQ ID NOS: 75
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APPLICANT: Majunder, Kumud
TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoding
FILB REFERENCE: 15966-721 US ...
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LOCATION: (20)
OTHER INFORMATION: Wherein Xaa is any amino acid as defined in
OTHER INFORMATION: specification
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ORGANISM: Homo sapiens
FEATURE:
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FILING DATE: 2000-03-17
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Shimkets, Richard:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vernet,
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Shimkets, Richard ?
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Vernet, Corine
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US-09-804-014A-74
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PRIOR FILLING DATE: 2000-03-10
PRIOR PELICATION NUMBER: 60/188,277
PRIOR PELICATION NUMBER: 60/189,277
PRIOR PELICATION NUMBER: 60/189,139
PRIOR APPLICATION NUMBER: 60/189,139
PRIOR PELICATION NUMBER: 60/189,140
PRIOR PELICATION NUMBER: 60/190,401
PRIOR APPLICATION NUMBER: 60/190,401
PRIOR APPLICATION NUMBER: 60/190,401
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PRIOR FILING DATE: 2000-03-10
PRIOR APPLICATION NUMBER: 60/189,139
PRIOR FILING DATE: 2000-03-14
PRIOR APPLICATION NUMBER: 60/189,140
PRIOR FILING DATE: 2000-03-14
PRIOR APPLICATION NUMBER: 60/190,401
                             NUMBER OF SEQ ID NOS: 75
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 74
LENGTH: 312
TYPE: no.
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LENGTH: 312
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PRIOR APPLICATION NUMBER: 60/
                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Shimkets, Richard
APPLICANT: Spaderna, Steven
APPLICANT: Majunder, Kunud
TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoding Same
FILE REFERENCE: 15966-721 US
CURRENT APPLICATION NUMBER: US/09/804,014A
CURRENT FILING DATE: 2002-04-24
CURRENT FILING DATE: 2002-04-24
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APPLICANT: Par
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PRIOR APPLICATION NUMBER: 60/190,231
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ORGANISM: Homo sapiens
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Fernandes,
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TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoding Same
FILE REFERENCE: 15966-721 US
CURRENT APPLICATION NUMBER: US/09/804,014A
CURRENT FILING DATE: 2002-04-24
PRIOR APPLICATION NUMBER: 60/188,316
PRIOR FILING DATE: 2000-03-10
PRIOR APPLICATION NUMBER: 60/188,277
PRIOR APPLICATION NUMBER: 60/189,277
PRIOR APPLICATION NUMBER: 60/189,277
PRIOR APPLICATION NUMBER: 60/189,139
PRIOR FILING DATE: 2000-03-16
PRIOR FILING DATE: 2000-03-14
PRIOR APPLICATION NUMBER: 60/189,140
PRIOR APPLICATION NUMBER: 60/199,401
PRIOR APPLICATION NUMBER: 60/190,401
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; ORGANISM: Homo mapiens
US-09-804-014A-39
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US-09-804-014A-39
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LENGTH: 1321
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Best Local (
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APPLICANT: Radigaru, Muralidhara
APPLICANT: Vernet, Corine
APPLICANT: Fernandes, Elma (1)
APPLICANT: Shimkets, Richard
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PRIOR FILING DATE: 2000-03-17.
NUMBER OF SEQ ID NOS: 75
SOFTWARE: Patentin Ver. 2.1
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                                                                     63 KVALVGLTAETSHALVPKEIPGKGGIWRVIFKPPDPDNTFLSRLNEFLAGEGMTVGELSR 122
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                                                                                                                                                                                                                                                                 91;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Vernet, Corine 4.
Fernandes, Elma 4.
Shimkets, Richard.
Spaderna, Steven/;
Majumder, Kumud
                                                                                                                                                                                                                                                                                     Similarity
ALGOBALSPATVPCISPELLAHLLGQAMAHAPQPLLP-MRYRKLRVFSGSAVPAPEBESF 180
                                                                                                NAVLLELLEDTDVSAIPSEVQGKGGVWKVIFKTPNQDTEFLERLNLFLEKEGQTVSGMFR 121
                                                                                                                                                                                            LALLEDWCRIMSVDEQKSLMVTGIPADFEEAEIQEVLQETLKSLGRYRLLGKIFRKQENA 61
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                                                                                                                                                                 LRLLEDWCRGMDMNPRKALLIAGISQSCSVAEIEEALQAGLAPLGEYRLLGRMFRRDENR 62
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                                                                                                                                                                                                                                                            43.8%; Score 436; DB 10; larity 46.9%; Pred. No. 2.7e-35; Conservative 530; Mismatches 71;
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46.9%; Pred. No. 2.6e-35;
tive 30; Mismatches 71;
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US-09-965-529-1
                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                   Sequence 16, Application US/09804014A Publication No. US20030064489A1
APPLICANT: Li, Li
APPLICANT: Padigaru, Muralidhara
APPLICANT: Vernet, Corine
APPLICANT: Vernet, Corine
APPLICANT: Fernandes, Elma
APPLICANT: Shimkets, Richard
APPLICANT: Spaderna, Steven
APPLICANT: Majumder, Kumud
TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoding
FILE REFERENCE: 15966-721 US
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ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20020182671A1 112301CD1
US-09-965-529-1
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FILE REFERENCE: PF-0731 USA
CURRENT APPLICATION UNMEBER: US/09/965,529
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION UNMER: 60/149,641; 60/164,203; PCT/US00/22315
PRIOR FILING DATE: 1999-08-17; 1999-11-09; 2000-08-14
RUMBER OF SEQ ID NOS: 74
SOFTWARE: PERL PROGRAM
SEQ ID NO 1
LENGTH: 351
TYPE: PRT
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Publication No. US20020182671A1
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APPLICANT: YUE, H
APPLICANT: TANG,
182 GRWMFHTTQMIKAW 195
                                             181 EVWLEQATEIVKEW 194
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                                                                                                                                                                                      63 KVALVGLTAETSHALVPKEIPGKGGIWRVIFKPPDPDNTFLSRLNEFLAGEGMTVGELSR
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                                                                                             ALGHENGSLDPEQGMIPEMWAPMLAQAL-EALQPALQCLKYKKLRVFSGRESPEPGEEEF
                                                                                                                              ALGQEALSPATVPCISPELLAHLLGQAMAHAPQPLLP-MRYRKLRVFSGSAVPAPEEESF
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PATTERSON, Chandra
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TANG, Y. Tom
BANDMAN, Olga
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AZIMZAI, Yalda
BAUGHN, Mariah R.
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46.9%; Pred. No. 3.1e-35;
vative 30; Mismatches 71
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APPLICANT: LAL, Preeti; YUE, Henry
APPLICANT: TANG, Y. Tom; BANDMAN, Olga
APPLICANT: BURFORD, Neil; AZIMZAI, Yalda
APPLICANT: BURFORD, Neil; AZIMZAI, Yalda
APPLICANT: BURGHY, Mariah R.; LU, Dyung Aina M.
APPLICANT: PATTERSON, Chandra
TITLE OF INVENTION: MEMBRANE ASSOCIATED PROTEINS
FILE REFERENCE: PP-0731-1 USA
CURRENT APPLICATION NUMBER: US/09/969,680A
CURRENT FILING DATE: 2001-10-02
PRIOR APPLICATION NUMBER: US/09/22315
PRIOR FILING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: 60/149,641
PRIOR APPLICATION NUMBER: 60/149,641
PRIOR APPLICATION NUMBER: 60/149,641
PRIOR FILING DATE: 1999-08-17
PRIOR FILING DATE: 1999-11-09
PRIOR FILING DATE: 1999-11-09
PRIOR FILING DATE: 1999-11-09
PRIOR FILING DATE: 1999-11-09
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US-09-969-680A-1
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US-09-804-014A-16
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PRIOR FILLING DATE: 2000-03-10
PRIOR PELLORITON NUMBER: 60/188,277
PRIOR FILLING DATE: 2000-03-10
PRIOR FILLING DATE: 2000-03-14
PRIOR APPLICATION NUMBER: 60/189,139
PRIOR FILLING DATE: 2000-03-14
PRIOR FILLING DATE: 2000-03-14
PRIOR APPLICATION NUMBER: 60/189,140
PRIOR APPLICATION NUMBER: 60/190,401
PRIOR APPLICATION NUMBER: 60/190,401
PRIOR FILLING DATE: 2000-03-17
PRIOR FILLING DATE: 2000-03-17
PRIOR FILLING DATE: 2000-03-17
PRIOR FILLING DATE: 2000-03-17
PRIOR FILING DATE: 2000-03-17
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PRIOR FILING DATE: 2000-03-17
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SEQ ID NO 16
LENGTH: 351
                                                                                                                                                                                                                                                                                                         SOFTWARE: PERL Program
SEQ ID NO 1
LENGTH: 351
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NAME/KBY: misc féature
OTHER INFORMATION: Incyte
D9-969-680A-1
                                                                                                                                                                                                       ORGANISM: Homo sapiens
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                                                        ID No. US20030124649A1 112301CD1
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US-10-341-434-10
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PRIOR FILING DATE: 2002-01-15
NUMBER OF SEQ ID NOS: 238
SOFTWARE: Patentin version 3.1
SEQ ID NO 10
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Publication No. US20030215835A1

GENERAL INFORMATION:
APPLICANT: Origene Technologies
APPLICANT: Origene Technologies
APPLICANT: Origene Technologies
FILE REFERENCE: 90 204 205 R1
CURRENT APPLICATION NUMBER: US/10/341,434
CURRENT FILING DATE: 2003-07-18
PRIOR APPLICATION NUMBER: US/10/341,434
CURRENT FILING DATE: 2003-01-15
PRIOR RELING DATE: 2002-01-15
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Best Local
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TYPE: PRT
ORGANISM: Homo sapiens
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                                                          182 GRWMFHTTQMIKAW 195
                                                                                                                                                                                                          63 KVALVGLTAETSHALVPKEIPGKGGIWRVIFKPPDPDNTFLSRLNEFLAGEGMTVGELSR
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l Similarity 46.9%;
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Pred. No. 3.1e-35;
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Search completed: April Job time: 44.5624 secs

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4 US-09-248-796A-20235
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US-09-949-016-10835
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Patent NO. 6387639
GENERAL INFORMATION:
APPLICANT: Jerome B. Posner
APPLICANT: Josep O. Dalmau
APPLICANT: Myrna R. Rosenfeld
TITLE OF INVENTION: Ma Family Polypeptides and
TITLE OF INVENTION: Antibodies
FILE REFERENCE: SLK98-01
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          Sequence 4, Application US/09189527A
Patent No. 6387639
GENERAL INFORMATION:
APPLICANT: Jerome B. Posner
APPLICANT: Josep O. Dalmau
APPLICANT: Myrna R. Rosenfeld
TITLE OF INVENTION: Ma Family Polypeptides and Anti-Ma
TITLE OF INVENTION: Mathematical Polypeptides and Anti-Ma
TITLE REFERENCE: SLK98-01
CURRENT APPLICATION NUMBER: US/09/189,527A
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CURRENT FILING DATE: 1998-11-10
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 13
LENGTH: 462
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Length 462;

Gape

125 273 Result No.

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Sequence 10835, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTEN: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307

CURRENT FILING DATE: 2000-04:14
PRIOR APPLICATION NUMBER: 00/241,755
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
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US 09-949-016-10835
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; TYPE: PRT
; ORGANISM: homo sapiens
US-09-189-527-4
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US-09-555-790A-2
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Matches
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LENGTH: 577
Sequence 2, Application US/0955790A
patent No. 6555632
GENERAL INFORMATION:
APPLICANT: 1TOH, KYOGO et al.
TITLE OF INVENTION: TUMOR ANTIGEN PEPTIDE DERIVATIVES
FILE REFERENCE: 0020-4716p
CURRENT APPLICATION NUMBER: US/09/555,790A
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NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
SEQ ID NO 4
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Best Local &
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-09-949-016-10835
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Local Similarity 46.6%; Pred. No. 1.5e-21;
neb 54; Conservative 25; Mismatches 30;
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                                                                                                                                                                                                                                                                                                53 YVLRLETLLRRAVEKRAİPRRIADQVRLEQVMAGATLN--QMLWCRLRELKD------
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Similarity 23.5%; Pred. No. 0.03;
36; Conservative '29; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LRRAVEKRAIPRRIADQVRLEQVWAGA----TLNQMLWCRLRELKDQGPPPSFLEL 112
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                                                                                                                                                                                                     EIQQPPPGPESYVPPYRPSLEEDSASLSGESLD
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US-09-202-047A-2
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                                                                                                                                 US-09-908-988B-4
                                                                                                                                                  RESULT 6
     GENERAL INFORMATION:
APPLICANT: OLSON, ERIC
APPLICANT: SPENCER, JEFFREY A.
APPLICANT: SPENCER, JEFFREY A.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR STABILIZING MICROTUBULES
TITLE OF INVENTION: IN STRIATED MUSCLE CELLS
                                                                                                                                                                                                                                                                                                                                                                                                                      Best Loc
Matches
                                                                                              Sequence 4, Application US/099089888 Patent No. 6740751
                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local (
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; LENGTH: 800
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-555-790A-2
                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Homo sapiens
US-09-202-047A-2
                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: ITOH, Kyogo
APPLICANT: SHICHLO, Shigeki
APPLICANT: SHICHLO, Shigeki
APPLICANT: IMAI, Yasuhisa
TITLE OF INVENTION: TUMOR ANTIGEN PROTEINS, GENES THEREFOR, AND TUMOR
TITLE OF INVENTION: ANTIGEN PEPTIDES
FILE REFERENCE: 0020-4491P
CURRENT APPLICATION NUMBER: US/09/202,047A
CURRENT APPLICATION NUMBER: US/09/202,047A
CURRENT FILING DATE: 1998-12-07
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PATENTIN VET. 2.1
SEQ ID NO 2
LENGTH: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/09202047A Patent No. 6815531 GENERAL INFORMATION:
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NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2
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Best Local Similarity
582 MDFERD-
                                        124 ASFENESIEEPEERDGYGRWNHEGDD 149
                                                                                     540 BEDE-----DPERKGAIVFNATSE---FCRTLGEIPTYG
                                                                                                                                                                          489 VLEEDEAELELQKQLE------KGRRLRQLQQLQQLRDSGEKVVEIVKKLESRQRGW 539
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                                                                                                                             65 VEKRAIPRRIADQVRLEQVMAGATLNQMLWCR-LRELKDQGPPPSFLELMKVIREEEEEE 123
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                                                                                                                                                                                                                       5 IVQADNPSISVEECLEAFKQVFGSLESRRTAQVRYLKPYQEEGEKVSAYVLRLETLLRRA 64
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602
                                                                                                                                                                                                                                                                                                              DB 4;
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                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Human
US-09-949-016-7561
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                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 39; Conserv
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APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION
FILE REFERENCE: CL001307
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Best Local Similarity
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CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR TIPLICATION NUMBER: 60/237,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE: MYOG:028US
CURRENT APPLICATION NUMBER: U$/09/908,988B
CURRENT FILING DATE: 2000-07-18
PRIOR APPLICATION NUMBER: 60/219,020
PRIOR FILING DATE: 2000-07-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
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SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 1307
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                                                                                                                                IVLKEKENELKRLEAMLKERESDLSSKTQLLQDVQDE-----NKLFKSQIEQLKQQN
                                                   YQQASSFPPHE -- ELLKVISEREKEISGLWNELDSLKDAVEHQRKKNNERQQQVEAVELE 1049
                                                                                                                                                                   ------LRLETLLRRAVEKRAIPRRIADQVRLEQVMAGATLNQMLWCRLRELKDQG 104
                                                                                                                                                                                                             EEQMNTMKAVLEEKEKDLANTGKWLQDLQEENESLKAHVQEVAQHNLKEASSASQFEELE
                                                                                         Conservative
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)S: 207012
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19.0%; Pred. No. 1.4;
active 25; Mismatches
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25.0%; Pred. No. 0.21;
ative 23; Mismatches
-GYGRWNH 145
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US-08-800-644-94
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Sequence 94, App. -
No. 5616500
Sequence 94, Application US/08800644 Patent No. 5958752
                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (714) 760-95
INFORMATION FOR SEQ ID NO:
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: FEGITICK, MINUSER: 36,799 REGISTRATION NUMBER: 36,799 REFERENCE/DOCKET NUMBER: NIH054.001A TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1060-0404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/0
FILING DATE: 30-APR-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Chung, Soo-Il
APPLICANT: Park, Sang-Chul
TITLE OF INVENTION: Trichohyalin and Transglutaminase-3 and
TITLE OF INVENTION: Mehods of Using Same
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                                                                                                                                  137 R 137
                                                                                                                                                                   614 EERLEQRLKREEVERL---EQEERRDE---
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                                                                                                                                                                                                                                                                                                                                                                                                                                1898 amino acids
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Pred. No. 5.4;
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GENERAL

INFORMATION:

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APPLICANT:

APPLICANT:

Kim, In-Gyu Chung, Soo-Il Steinert, Peter

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Best Local (
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                                                                    CURRENT APPLICATION NUMBER: US/09/538,092
CURRENT FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: 60/127,352
PRIOR FILING DATE: 1999-04-01
PRIOR APPLICATION NUMBER: 60/178,965
PRIOR FILING DATE: 2000-02-01
                                                                                                                                                                                                                                                                                    APPLICANT: Giot Loic
APPLICANT: Mansfield, Traci A.
TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
FILE REFERENCE: 15966-542
                                  NUMBER OF SEQ ID NOS: 1387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (714) 760-9502 INFORMATION FOR SEQ ID NO: 9
SOFTWARE: CuraPatSeqFormatter Version 0.9
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APPLICATION NUMBER: US 08
FILING DATE: 30-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: PROJECT NO STATE NO 
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 1898 amino acid
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REGISTRATION NUMBER: 36,799
REFERENCE/DOCKET NUMBER: .NII
TELECOMMUNICATION INFORMATION:
TELEPHONE: (714) 760-0404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
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ITLE OF INVENTION: Trichchyalin and Transglutaminase-3 and
ITLE OF INVENTION: Mehodsfof Using Same
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35; Conserv
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.620 Newport Center Drive, Sixteenth Floor
Newport Beach
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Pred. No. 5.4;
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RESULT 12
US-09-949-016-10896
US-09-949-016-10896
Sequence 10896, Application US/09949016
Sequence 10896, Application US/09949016
Patent No. 6812339
Sequence 10896, Application
US/09949016
Seque
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US-09-248-796A-20235
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LENGTH: 531
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APPLICANT: Keith Weinstock et al
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICA
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/248,796A CURRENT FILING DATE: 1999-02-12 PRIOR APPLICATION NUMBER: US 60/074,725 PRIOR EILING DATE: 1998-02-13 PRIOR APPLICATION NUMBER: US 60/096,409 PRIOR FILING DATE: 1998-08-13
                                  CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 28208
                                                                                                      FILE REFERENCE: CL001307
PRIOR APPLICATION NUMBER: 60/241,755
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NAME/KEY: misc_feature
LOCATION: (0)...(0)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         661 R 661
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   110 -----LELMKVIREEEEEEASFENESIEEPEERDGYGRWNHEGD 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20235,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66 ITELEEGRRIEKERREQLKLQKQQERQEALARGEIVEDDDEMDEDDQ--EEGD 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20 EAFKQVFGSLESRRTAQVR---YLKPYQEEGEKVSAYVLRLETLLRRAVEKRAIPRRIAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       56 RLETLLRRAVEKRAIPRRIADQVRLEQVMAGATLNQMLWCRLRELKDQGPPPSF-----
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Pred. No. 1.1;
21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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US-09-538-092-1130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: FastSEQ for Windows Version SEQ ID NO 10896
LENGTH: 568
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                                                                                                                                                                                                                                       Query Match
Best Local
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Patent No. 6753314
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APPLICANT: Glot, Loic
APPLICANT: Mansfield, Traci A.
TITLE OF INVENTION: Protein-Protein Complexes and I
FILE REFERENCE: 15966-542
CURRENT APPLICATION NUMBER: US/09/538,092
CURRENT APPLICATION NUMBER: 60/127,352
PRIOR APPLICATION NUMBER: 60/127,352
PRIOR FILING DATE: 1999-04-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 1387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 60/178,965 PRIOR FILING DATE: 2000-02-01
                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
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365
                                    120
                                                                                                                                               253 AVAMAETIKTIROVEVINĘGDCIVRSKGAVAIADAIRGGIPKIKELNISFCEIKRDÁA-- 310
                                                                                                                                                                                   12 SISVEECLEAFKQV----FGSLESRRTAQVRYLKPYQEEGEKVSAYVLRLETLLRRAVEK 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          68 RAIPRRIADQVRLEQV-MAGATLNQMLWCRLRELKDQGPPPSFLELMKVIR-----EE 119
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                                                                        LAVAEAMADKAELEKLDLNGNTLGEEGCEQLQEVLEG---
                                                                                                           RAIPRRIADQVRLEQV-MAGATLNQMLWCRLRELKDQGPPPSFLELMKVIR-----EE 119
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22;
                                                                                                                                                                                                                    22; Mismatches
 383
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; TYPE: PRT
; ORGANISM: SchizoBaccharomyces pombe
US-09-540-824-26
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APPLICANT: Thiele, Dennis
APPLICANT: Liu, Phillip
TITLE OF INVENTION: No.
FILE REFERENCE: UM-04266
                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 1387
SOFTWARE: CuraPatSeqFormatter Version
SEQ ID NO 1285
LENGTH: 620
TYPE: PRT
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SEQ ID NO 26
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Patent No. 6753314
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Patent No. 6383753
                                                                                                       Query Match
Best Local
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CURRENT FILING DATE: 2000-03-31
NUMBER OF SEQ ID NOS: 28
                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: 15966-542
CURRENT APPLICATION NUMBER: US/09/538,092
CURRENT FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: 60/127,352
PRIOR FILING DATE: 1999-04-01
PRIOR FILING DATE: 1999-04-01
PRIOR APPLICATION NUMBER: 60/178,965
PRIOR FILING DATE: 2000-02-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Giot, APPLICANT: Mansi
                                                                                                                                                                              ORGANISM: Homo sapiens
FEATURE:
FEATURE:
NAME/KEY: misc_feature
LOCATION: (0)...(0)
OTHER INFORMATION: Polypeptide Accession Number Q08379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PPLICANT: Mansfield, Traci A.
ITLE OF INVENTION: Protein-Protein Complexes and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Match 10.4%; Score 80; DB 3; Local Similarity 25.8%; Pred. No. 2.4;
                                                                                                     Local
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  212 LKETVELKSQEAQSLQQQRDQYLGHLQQY-----VAAYQQLTSEKEVLHNQLLLQTQLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              88 TLNQMLWCRLRELKDQGPPPSFLELMKVIR-EEEEEEASFENESIEEPEERD---GYGR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30 ESRRTAQVRYLKPYQEEGEKVSAYVLRLETLLRRAV-EKRAIP-RRIADQVRLEQVMAGA 87
                                           15 VEECLEAFKQVFGSLESRRTAQVRYLKPYQEEGEKVSAY------VLRLETLLRRAV- 65
                                                                                                       Similarity
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                                                                                    Conservative
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                                                                                  10.1%; Score 77.5; I
25.0%; Pred. No. 3.2;
tive 26; Mismatches
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                                                                                                                           DB 4; Length 620;
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                                                                                    48; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Method
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of Using Same
                                                                                    31;
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                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         305
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Search completed: April 8, 2005,,12:52:55
Job time : 11.4454 sece
                                          266 DQLQQQEAQGKAVAEMARQELQETQERLEAATQQNQQLRAQLSLMAHPG-----EGDGL 319
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Post-processing: Minimum Match 05 Maximum Match 100%

Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence:
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OM protein - protein search, using sw model
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                                                                                                                                                                                                                                                                                                                                                                                                   pred. No. is the number of score greater than or equal and is derived by analysis
                                                                                                                                                                                                                                                                                                  Score
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766
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1486.133 Million cell updates/sec
                                                                                                                                                                                                                                                                                                  Match
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                                                                                                                                                                                                                                                                                                                                                                                 is the number of results predicted by chance to have a ter than or equalito the score of the result being printed, ived by analysis of the total score distribution.
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Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /cgn2 6/ptodata/1/pubpaa/US09B PUBCOMB.pep:*
/cgn2 6/ptodata/1/pubpaa/US09C PUBCOMB.pep:*
/cgn2 6/ptodata/1/pubpaa/US09 NEW PUB.pep:*
/cgn2 6/ptodata/1/pubpaa/US10A PUBCOMB.pep:*
/cgn2 6/ptodata/1/pubpaa/US10B PUBCOMB.pep:*
/cgn2 6/ptodata/1/pubpaa/US10C PUBCOMB.pep:*
/cgn2 6/ptodata/1/pubpaa/US10D PUBCOMB.pep:*
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cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
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6/ptodaţa/1/pubpaa/US06_PUBCOMB.pep:*
6/ptodaţa/1/pubpaa/US07_NEW FUB.pep:*
6/ptodaţa/1/pubpaa/PCTUS_PUBCOMB.pep:*
6/ptodaţa/1/pubpaa/US08_NEW FUB.pep:*
6/ptodaţa/1/pubpaa/US08_PUBCOMB.pep:*
                                                                                                                                                                                        13 ** US-10-037-860-9
13 ** US-10-037-860-11
13 ** JUS-10-037-860-13
9 ** US-09-965-529-7
                                                                                                                                                                                                                                                                                                  DB . ID
                                                                                                                        10 US-09-969-680A-7
16 US-10-408-765A-2385
15 US-10-094-749-1978
                                         US-09-804-014A-16
US-09-869-680A-1
US-10-341-434-10
                                                                                                       US-09-965-529-1
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Sequence 9, Appli
Sequence 11, Appl
Sequence 7, Appli
Sequence 7, Appli
Sequence 7, Appli
Sequence 2385, Ap
Sequence 1978, Ap
Sequence 1, Appli
Sequence 16, Appli
Sequence 11, Appli
Sequence 1, Appli
Sequence 4, Appli
Sequence 4, Appli
Sequence 4, Appli
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45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	
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US-10-380-492A-4	-363-616-44	10-437-963-	-10-839-016-3	09-866-582-33	-10-437-963-182	-10-437-963-18	-10-437-963-187	-10-298-417-	-723-51	-10-408-	-10-775-627	US-10-775-649-4	9-808-9	-10-437-963-12973	-10-437-963-1875	US-10-959-539-51	-10-921-110-	-754-829A	-10-416-477	-10-438-	-10-310-154-	-10-437-963-15	-10-755-889-	1	-10-094-749-	-09-804-014A-7	US-09-804-014A-73	-804-014A-3	39-2	-296-	94-466-3	
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# ALIGNMENTS

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; TYPE: PRT
; ORGANISM: homo sapiens
US-10-037-860-9
                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 9
                                                                                                                                                                                                                        Query Match 100.0%; Score 766; DB 13; Best Local Similarity 100.0%; Pred. No. 4.9e-70; Matches 149; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Jerome B. Posner
APPLICANT: Josep O. Dalmau
APPLICANT: Myrna R. Rosenfeld
APPLICANT: Myrna R. Rosenfeld
TITLE OF INVENTION: MA FAMILY POLYPEPTIDES AND ANTI-MA
TITLE OF INVENTION: ANTI-BODIES
FILE REPERENCE: 2581.1004-004
CURRENT APPLICATION NUMBER: US/10/037,860
CURRENT APPLICATION NUMBER: 09/189,527
PRIOR APPLICATION NUMBER: 09/189,527
PRIOR PILING DATE: 1998-11-10
121 EEEASFENESIEEPEERDGYGRWNHEGDD 149
                                                                        61 LRRAVEKRAIPRRIADQVRLEQVMAGATLNQMLWCRLRELKDQGPPPSFLELMKVIREEE 120
                                                                                                                                    1 DLMHIVQADNPSISVEECLEAFKQVFGSLESRRTAQVRYLKPYQEEGEKVSAYVLRLETL
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                                                                                                                                                                                                                                                                           Length 149;
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121

BEEASFENESIEEPEERDGYGRWNHEGDD 149

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APPLICANT: Jerome B. Posner
APPLICANT: Josep O. Dalnau
Yurna R. Rosenfeld
TITLE OF INVENTION: MA FAMILY POLYPEPTIDES AND ANTI-MA
TITLE OF INVENTION: MA FAMILY POLYPEPTIDES AND ANTI-MA
TITLE OF INVENTION: MATIBODIES
FILE REFERENCES: 2581.1004-004
CURRENT APPLICATION NUMBER: US/10/037,860
CURRENT EPLING DATE: 2001-01-04
PRIOR APPLICATION NUMBER: 09/10/95,527
PRIOR FILING DATE: 1998-11-10
NUMBER OF SEQ ID NOS: 14
SOSTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 11
LENGTH: 283
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; ORGANISM: homo sapiens
US-10-037-860-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 13, Applica Publication No. US20 GENERAL INFORMATION:
                                                             Query Match
Best Local Similarity
Matches 68; Conserv
                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/10/037,860
CURRENT FILING DATE: 2001-01-04
PRIOR APPLICATION NUMBER: 09/189,527
PRIOR FILING DATE: 1998-11-10
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 147; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 98.6%; Score 755; DB 13; Best Local Similarity 98.7%; Pred. No. 1.5e-68;
                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Jerome B. Posner
APPLICANT: Josep O. Dalmau
APPLICANT: Myrna R. Rosenfeld
TITLE OF INVENTION: MA FAMILY POLYPEPTIDES AND ANTI-MA
FILE REFERENCE: 2581.1004-004
                                                                                                                                                                                                                                       LENGTH: 463
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            135 DLMHIVQADNPSISVEECLEAFKQVFGSLESRRTAQVRYLKTYQEEGEKVSAYVLRLETL 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 LRRAVEKRAIPRRIADQVRLEQVMAGATLNQMLWCRLRELKDQGPPPSFLELMKVIREEE 120
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6 VQADNPSISVEECLEAFKQVFGSLESRRTAQVRYLKPYQEEGEKVSAYVLRLETLLRRAV 65
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                                                                       Conservative
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                                                   42.2%; Score 323; DB 13; 52.7%; Fred. No. 3e-24; ative 26; Mismatches 33;
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                                                                                                                 DB 13; Length 463;
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                                                                       Gaps
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GENERAL INFORMATION:

APPLICANT: LAL, Preeti; YUE, Henry
APPLICANT: LAWG, Y. Tom; BANDMAN, Olga
APPLICANT: BURFORD, Neil; AZIMZAI, Yalda
APPLICANT: BAUGHN, Mariah R.; LU, Dyung Aina M.
APPLICANT: BAUGHN, Mariah R.; LU, Dyung Aina M.
APPLICANT: PATTERSON, Chandra
TITLE OF INVENTION: MEMBRANE ASSOCIATED PROTEINS
FILE REFERENCE: PF-0731-1 USA
CURRENT APPLICATION UNDER: US/09/969,680A
CURRENT PFILING DATE: 2001-10-02
                                                                                                                                                                                                                                                                           RESULT 5
US-09-969-680A-7
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; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20020182671A1 2483172CD1
US-09-965-529-7
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CURRENT FILING DATE: 2001-09-26
ERIOR APPLICATION NUMBER: 60/149,641; 60/164,203; PCT/US00/22315
PRIOR FILING DATE: 1999-68-17; 1999-11-09; 2000-08-14
NUMBER OF SEQ ID NOS: 74
SOPTWARE: PERL Program
SEQ ID NO 7
LENGTH: 353
TYPE: PRT
                                                                                                                                                                                                                              Sequence 7, Application US/09969680A Publication No. US20030124649A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 7, Application US/09965529
Publication No. US20020182671A1
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APPLICANT: YUE, Henry
APPLICANT: TANG, Y. To
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE: PF-0731 USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: MEMBRANE ASSOCIATED PROTEINS
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Local Similarity 46.3%;
hes 62; Conservative 29
                                                                                                                                                                                                                                                                                                                                                                      329
                                                                                                                                                                                                                                                                                                                                                                                                                                                              272 LQKVVEKGÁIDKDNVNQÁRLEQVIÁGÁNHSGAIRRQLWL---TGAGEGPAPNLFQLLVQI 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     340 LGPDRESLE 348
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 LRRAYEKRAIPRRIADOVRLEOVMAGA----TUNOMUMCRLRELKDOGPPPSFLELMKVI 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 DLMHIVQADNPSISVEECLEAFKQVFGSLESRRTAQVRYLKPYQEEGEKVSAYVLRLETL 60
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BANDMAN, Olga
BURFORD, Neil
AZIMZAI, Yalda
BAUGHN, Mariah R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REEEAKEEEEEAEA 342
                                                                                                                                                                                                                                                                                                                                                                                                                 REEEEEEASFENES 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 295.5; DB 9; Length 353;
Pred. No. 1.3e-21;
9; Mismatches 36; Indels 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7;
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GENERAL INFORMATION:

APPLICANT: Ghosh, Soumitra S.

APPLICANT: Fahy, Boin D.

APPLICANT: Zhang, Bing
APPLICANT: Taylor, Steven W.

APPLICANT: Taylor, Steven W.

APPLICANT: Glenn, Gary M.

APPLICANT: Warnock, Daie E.

TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
FILE REFERENCE: 660088.465

FURRENT APPLICATION NUMBER: US/10/408,765A
CURRENT APPLICATION NUMBER: US/10/408,765A
CURRENT FILING DATE: 2003-04-04
NUMBER OF SEG ID NOS: 3077
SOFTWARE: FastSEQ for Windows Version 4.0

SEG ID NO 2385
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US-10-408-765A-2385
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; ORGANISM: Homo sapiens
US-10-408-765A-2385
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PRIOR FILING DATE: 2000-08-14
PRIOR PELICATION NUMBER: 60/149,641
PRIOR FILING DATE: 1999-08-17
PRIOR APPLICATION NUMBER: 60/164,203
PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 74
SOFTWARE: PERL Program
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2385, Application US/10408765A Publication No. US20040101874A1
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                                                                                                                                                                                                                  Query Match 37.5%; Score 287; DB 16; Best Local Similarity 43.8%; Fred. No. 1.4e-20; Matches 63; Conservative 30; Mismatches 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 38.6%; Score 295.5; DB 1 Best Local Similarity 46.3%; Pred. No. 1.3e-21;
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ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature ;
OTHER INFORMATION: Incyte ID No. US20030124649A1 2483172CD1
                                                                                                                                                                                                                                                                                                                                                              LENGTH: 452
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                      122
                                                              275
                                                                                                                                       215 IMRVLQANNOSITVEQCLDALKQIFGDKEDFRASQFRFLQTSPKIGEKVSTFLLRLEPLL 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 LRRAVEKRAIPRRIADQVRLEQVMAGA----TLNQMLWCRLRELKDQGPPPSFLELMKVI 116
                                                          1 DIMHIVQADNPSISVEECLEAFKQVFGSLESRRTAQVRYLKPYQEEGEKVSAYVLRLETL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62;
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---EEASFENESIEEPEERDGYGR 142
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APPLICANT: LAL, Preeti
APPLICANT: YUB, Henry
APPLICANT: TANG, Y. TON
APPLICANT: BANDMAN, O1c
APPLICANT: BURFORD, Nei
APPLICANT: BURFORD, Nei
APPLICANT: BURFORD, Nei
APPLICANT: BAUGHN, Mari

TANG, Y. Tom
BANDMAN, Olga
BURFORD, Neil
AZIMZAI, Yalda
BAUGHN, Mariah R.
LU, Dyung Aina M.
PATTERSON, Chandra

APPLICANT:

Sequence 1, Application US/09965529 Publication No. US20020182671A1

GENERAL INFORMATION:

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CURRENT APPLICATION NUMBER: US/10/094,749
CURRENT FILING DATE: 2002-03-12
PRIOR APPLICATION NUMBER: 60/350,435
PRIOR FILING DATE: 2002-01-24
PRIOR APPLICATION NUMBER: JP 2001-328381
PRIOR APPLICATION NUMBER: JP 2001-328381
PRIOR FILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 3381
SOFTWARE: PAtentIN Ver. 2.1
SEQ ID NO 1978
LENGTH: 399
TYPE: PRT
ORGANISM: Homo sapiens
US-10-094-749-1978
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RESULT 8
US-09-965-529-1
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APPLICANT:
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APPLICANT:
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: NAGAHARI, KENJI
APPLICANT: MASUHO, YASUHIKO
TITLE OF INVENTION: NOVEL FULL-LENGTH cDNA
FILE REFERENCE: 084335/0160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
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                                                                                                                                                                                                                                                                Local
                                                              328 WEASLARSVRAQTQEGAG
                                                                                                                        268 QKAMEKEALARASADRVRIROMLTRAHLTEPLDEALRKLRMAGRSPSFLEMLGLVRESEA 327
                                                                                                                                                                                      335 WENTEAVMKNK----EKPSGRGR
                                                                                           122 EEASFENESIEEPEERDG 139
                                                                                                                                                 62 RRAVEKRAIPRRIADQVRLEQVMAGATLNQMLWCRLRELKDQGPPPSFLELMKVIREEEE 121
                                                                                                                                                                                                    60;
                                                                                                                                                                                                                                                h 36.2%; Score 277; DB 15; Similarity 43.5%; Pred. No. 1.2e-19; 60; Conservative 30; Mismatches 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HIO, YURI
OTSUKA, KAORU
NAGAI, KEIICHI
IRIE, RYOTARO
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WAKAMATSU, AI
SATO, HIROYUKI
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YOSHIKAWA, TSUTOMU
OTSUKA, MOTOYUKI
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                                                              345
                                                                                                                                                                                                                                                                             Length 399;
                                                                                                                                                                                                                                                   Indels
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                                                                                                                                                                                         267
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APPLICANT: Fernandes, Elma
APPLICANT: Shimkets, Richard'
APPLICANT: Spaderna, Steven
APPLICANT: Spaderna, Steven
APPLICANT: Majumder, Kumud
TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoding Same
FILE REFERENCE: 15966-721 US
CURRENT APPLICATION NUMBER: US/09/804,014A
CURRENT FILING DATE: 2002-04-24
PRIOR APPLICATION NUMBER: 60/188,316
PRIOR FILING DATE: 2000-03-10
PRIOR APPLICATION NUMBER: 60/189,139
PRIOR APPLICATION NUMBER: 60/189,139
PRIOR APPLICATION NUMBER: 60/189,139
PRIOR APPLICATION NUMBER: 60/189,140
PRIOR APPLICATION NUMBER: 60/190,401
PRIOR APPLICATION NUMBER: 60/190,401
PRIOR APPLICATION NUMBER: 60/190,401
PRIOR FILING DATE: 2000-03-14
PRIOR APPLICATION NUMBER: 60/190,401
PRIOR FILING DATE: 2000-03-14
PRIOR APPLICATION NUMBER: 60/190,401
PRIOR FILING DATE: 2000-03-17
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                                                                                                       TYPE: PRT
ORGANISM: Homo sapiens
US-09-804-014A-16
                Query Match
Best Local S
Matches 58
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FILE REFERENCE: PF-0731 USA
CURRENT APPLICATION NUMBER: U3/09/965,529
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 60/149,641; 60/164,203; PCT/US00/22315
PRIOR FILING DATE: 1999-08-17; 1999-11-09; 2000-08-14
NUMBER OF SEQ ID NOS: 74
SOFTWARE: PERL Program
SEQ ID NO 1
LENGTH: 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 16, Application US/09804014A Publication No. US20030064489AL
                                                                                                                                                                     SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 16
LENGTH: 351
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                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 75
                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 60/190,231 PRIOR FILING DATE: 2000-03-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Incyte ID No. US20020182671A1 112301CD
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y Match 35.4%; Score 271.5; DB 10; Length 351; Local Similarity 44.6%; Pred. No. 3.7e-19; hes 58; Conservative 32; Mismatches 29; Indels 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
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Vernet, Corine
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                  11;
                  Gaps
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RESULT 11

US-10-341-434-10

US-10-341-434-10

Sequence 10, Application US/10341434

Publication No. US20030215835A1

GENERAL INFORMATION:
APPLICANT: Oridene Technologies

TITLE OF INVENTION: Differentially Regulated Profile REFERENCE: 9U 204 205 R1

CURRENT APPLICATION NUMBER: US/10/341,434

CURRENT EILING DATE: 2003-07-18
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APPLICANT: TANG, Y. Tom; BANDMAN, Olga
APPLICANT: BURFORD, Neil; AZIMZAI, Yalda
APPLICANT: BUUGHN, MATIAH R.; LU, Dyung Aina M.
APPLICANT: BAUGHN, MATIAH R.; LU, Dyung Aina M.
APPLICANT: PATTERSON, CHANDRA
TITLE OF INVENTION: MEMBRANE ASSOCIATED PROTEINS
FILE REFERENCE: PF-0731-1 USA
CURRENT APPLICATION NUMBER: US/09/969,680A
CURRENT FILING DATE: 2001-10-02
PRIOR APPLICATION NUMBER: US/022315
PRIOR FILING DATE: 2000-08-14
PRIOR FILING DATE: 1999-08-17
PRIOR APPLICATION NUMBER: 60/149,641
PRIOR APPLICATION NUMBER: 60/164,203
PRIOR FILING DATE: 1999-11-09
NUMBER OF SEO ID NOS: 74
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SOFTWARE: PERL Program
SEQ ID NO 1
LENGTH: 351
TYPE: PRT
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; OTHER INFORMATION: Incyte ID No. US20030124649A1 112301CD1
US-09-969-680A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 10
US-09-969-680A-1
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/09969680A Publication No. US20030124649A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
PRIOR APPLICATION NUMBER: US 60/348,164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
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US-10-341-434-10
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SEQ ID NO 10
LENGTH: 351
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APPLICANT: Jerome B. Posner
APPLICANT: Josep O. Dalmau
APPLICANT: Myrna R. Rosenfeld
TITLE OF INVENTION: ANTIBODIES
TITLE OF INVENTION: ANTIBODIES
FILS REFERENCE: 2581.1004-004.
                                            Sequence 40, Application US/09804014A publication No. US20030064489A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4, Application US/10037860 Publication No. US20020123114A1
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Best Local Similarity
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PRIOR FILING DATE: 1998-11-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT FILING DATE: '2001-01-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR FILING DATE: 2002-01-15
PRIOR APPLICATION NUMBER: US
PRIOR FILING DATE: 2002-01-15
                               APPLICANT: Li, Li
                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 329
TYPE: PRT
ORGANISM: homo sapiens
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                                                                                                                                                                      272
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                                                                                                                                                                                                     61 LRRAVEKRAIPRRIADOVRIEOVMAGA----TLNOMLWCRLRELKDQGPPPSFLEL 112
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                                                                                                                                                                      LQKVVEKGAIDKDNVNQARLEQVIAGANHSGAIRRQLWL-
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Padigaru, Muralidhara
Vernet, Corine
                                                                                                                                                                                                                                                                                                          Conservative
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'S: 238
                                                                                                                                                                                                                                                                                            33.5%; Score 256.5; DB 1:
46.6%; Pred. No. 1.2e-17;
tive 25; Mismatches 30
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; OTHER INFORMATION: wherein Xaa is ; OTHER INFORMATION: specification US-09-804-014A-40
              CURRENT APPLICATION NUMBER: US/10/094,466
CURRENT FILING DATE: 2002-03-07
PRIOR APPLICATION NUMBER: 60/274,281
PRIOR FILING DATE: 2001-03-08
PRIOR PPLICATION NUMBER: 60/288,148
PRIOR APPLICATION NUMBER: 60/274,849
PRIOR PPLICATION NUMBER: 60/274,849
PRIOR FILING DATE: 2001-03-09
PRIOR APPLICATION NUMBER: 60/275,235
PRIOR FILING DATE: 2001-03-12
PRIOR PPLICATION NUMBER: 60/338,375
PRIOR FILING DATE: 2001-03-12
PRIOR PPLICATION NUMBER: 60/275,579
PRIOR APPLICATION NUMBER: 60/275,579
PRIOR APPLICATION NUMBER: 60/335,302
PRIOR APPLICATION NUMBER: 60/335,302
PRIOR PPLICATION NUMBER: 60/335,302
PRIOR PPLICATION NUMBER: 60/335,302
PRIOR PILING DATE: 2001-03-13
PRIOR PPLICATION NUMBER: 60/335,302
PRIOR PRILING DATE: 2001-10-31
PRIOR PPLICATION NUMBER: 60/335,302
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PRIOR FILING DATE: 2000-03-10
PRIOR APPLICATION NUMBER: 60/188,277
PRIOR FILING DATE: 2000-03-10
PRIOR FILING DATE: 2000-03-10
PRIOR FILING DATE: 2000-03-14
PRIOR APPLICATION NUMBER: 60/189,139
PRIOR FILING DATE: 2000-03-14
PRIOR PPLICATION NUMBER: 60/190,401
PRIOR PPLICATION NUMBER: 60/190,401
PRIOR PILING DATE: 2000-03-17
PRIOR APPLICATION NUMBER: 60/190,231
PRIOR FILING DATE: 2000-03-17
PRIOR APPLICATION NUMBER: 60/190,231
PRIOR FILING DATE: 2000-03-17
PRIOR FILING DATE: 2000-03-17
PRIOR PILING DATE: 2000-03-17
PRIOR FILING DATE: 2000-03-17
PRIOR FILING DATE: 2000-03-17
PRIOR FILING DATE: 2000-03-17
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APPLICANT: Spytek et al.
TITLE OF INVENTION: NOVEL HUMAN PROTEINS,
TITLE OF INVENTION: AND METHODS OF USING
TITLE OF INVENTION: THE SAME
FILE REFERENCE: 21402-290D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 38, Application US/10094466 Publication No. US20030203363A1
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TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoding
FILE REFERENCE: 15966-721 US
CURRENT APPLICATION NUMBER: US/09/804,014A
CURRENT FILING DATE: 2002-04-24
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TYPE: PRT
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LOCATION: (20)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              h 33.3%; Score 255; DB 10; Similarity 51.0%; Pred. No. 1.6e-17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LQKVVEKGAIDKDNVNQARLEQVIAGANHSGAIRRQLW 309
CATION NUMBER: 60/275,601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Shimkets,
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Sequence 1208, Application US/10296115

Publication No. US20040053248A1

GENERAL INFORMATION:
APPLICANT: Hyseq Inc

TITLE OF INVENTION: No. US20040053248A1e1 Nucleic Acids and Polypeptides

FILE REFERENCE: 784PCT

CURRENT APPLICATION NUMBER: US/10/296,115

CURRENT FILING DATE: 2002-11-18

PRIOR APPLICATION NUMBER: US/9/488,725

PRIOR FILING DATE: 2000-01-21

PRIOR FILING DATE: 2000-01-21

PRIOR APPLICATION NUMBER: US09/552,317

PRIOR FILING DATE: 2000-04-25

NUMBER OF SEQ ID NOS: 1478

SEQ ID NO 1208

LENGTH: 337

TYPE: PRT
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Search completed: April 8, 2003; Job time: 34.2861 Becs
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-094-466-38
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PRIOR FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: 60/277,338
PRIOR FILING DATE: 2001-03-20
Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 114
SOFTWARE: Patin 2.1
1500-038
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                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Homo sapiens -10-296-115-1208
                                                                                                                                                                                                                                                                                                                                       y Match 31.3%; Score 240; DB 15; Length 337;
Local Similarity 37.2%; Pred. No.'5.8e-16;
hes 54; Conservative 34; Mismatches 45; Indels 11
                                                                                                                                                                   140 LQNAIQAGIIAEKDANRTRLQQLLLGGELSRDLRLRLKDFLRMYANEQERLPNFLELIKM 199
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                                                                               200 VREEEDWDDAFIKRKRPKRSESMVE 224
                                                                                                                             116 IREEEEEASF-----ENESIEE 133
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                                                                                                                                                                                                                                                     61 LRRAVEKRAIPRRIADQVRLEQVMAGATLNQMLWCRLREL-----KDQGPPPSFLELMKV 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 LRRAVEKRAIPRRIADQVRLEQVMAGATLNQMLWCRLREL----KDQGPPPSFLELMKV 115
                      13:35:14
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Scoring table:
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                                                                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                 Published Applications AA:*

1: /cgn2_6/ptodata/1/pubpaa/US07 PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/US06 NEW PUB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US06 NEW PUB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/US07 NEW PUB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/US07 NEW PUB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/US08 NEW PUB.pep:*

8: /cgn2_6/ptodata/1/pubpaa/US08 PUBCOMB.pep:*

9: /cgn2_6/ptodata/1/pubpaa/US08 PUBCOMB.pep:*

10: /cgn2_6/ptodata/1/pubpaa/US09B PUBCOMB.pep:*

11: /cgn2_6/ptodata/1/pubpaa/US09C PUBCOMB.pep:*

12: /cgn2_6/ptodata/1/pubpaa/US09C PUBCOMB.pep:*

13: /cgn2_6/ptodata/1/pubpaa/US09C PUBCOMB.pep:*

14: /cgn2_6/ptodata/1/pubpaa/US10B PUBCOMB.pep:*

15: /cgn2_6/ptodata/1/pubpaa/US10B PUBCOMB.pep:*

16: /cgn2_6/ptodata/1/pubpaa/US10D PUBCOMB.pep:*

16: /cgn2_6/ptodata/1/pubpaa/US10D PUBCOMB.pep:*

17: /cgn2_6/ptodata/1/pubpaa/US10 NEW PUB.pep:*

18: /cgn2_6/ptodata/1/pubpaa/US10 NEW PUB.pep:*

19: /cgn2_6/ptodata/1/pubpaa/US10 NEW PUB.pep:*
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Gapop 10.0 , Gapext 0.5
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Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                  SUMMARIES
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De	562.5	593	596.5 596.5	596.5	518.5		score
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Description  Sequence 11, Appli Sequence 9, Appli Sequence 7, Appli Sequence 13, Appli Sequence 13, Appli Sequence 14, Appli Sequence 16, Appli Sequence 17, Appli Sequence 18, Appli Sequence 19, Appli Sequence 19, Appli Sequence 4, Appli Sequence 4, Appli	US-09-804-014A-40	TIS-10-037-860-7	.\US-09-804-014A-16 .\US-09-969-680A-1 .US-10-341-434-10	US-09-965-529-1	US-10-969-680A-7 US-10-037-860-13	:.US-10-037-860-11 :.US-10-037-860-9 :.US-09-965-529-7	B <sup>-</sup>
	Sequence 4, Appl Sequence 40, Appl	Sequence 7, Appli	sequence 16, Appl Sequence 1, Appli Sequence 10, Appl	Sequence 1, Appli	Sequence 7, Appli Sequence 13, Appl	Sequence 11, Appl Sequence 9, Appli Sequence 7, Appli	Description
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-10-420-845-	-10-220-381-	0-424-599-2686	4-7171	-10-037-417-5	-83	-080-334-1	σ,	0	0-128-714-	US-09-764-891-4172	8	-10	-10-282-122A-6794	-10-205	-10-	-10-158	-09-764	-10-221	-10-291	-10-082	US-10-408-765A-2992	-09-804-0142	-10-029-386-33	-09-804-014A-4	-10-	-10-959-	-10-094-466-	US-10-094-749-1978	;	US-09-804-014A-73	US-09-804-014A-39
22,	e 12, A	e 26866	e 7171	e 59, 1	e 838,	e 166, A	e 162:	e 1	e 820'	4172,	Sequence 34645, A	e 6065	e 67949,	e 57, A	Sequence 2246, Ap	e 197,	e 686,	e 355,	355,	260,	2992	41, A	33747,	42,	1208, A	26,	38,	e 197	e 74,	Sequence 73, Appl	Sequence 39, Appl

### ALIGNMENTS

180	QY 121 KKRWLAESLRGPALDLMHIVQADNPSISVEECLEAFKQVFGSLESRRTAQVRYLKTYQEE
120	Db 61 LAHLIGQAMAHAPQPLLPMRYRKLRVFSGSAVPAPEEESFEVWILEQATEIVKEWPVTEAE
120	QY 61 LAHLLGQAMAHAPQPLLPMRYRKLRVFSGSAVPAPEEESFEVWLEQATEIVKEWPVTEAE
60	Db 1 VQGKGGVWKVIFKTPNQDTEFLERLNLFLEKEGQTVSGMFRALGQEGVSPATVPCISPEL
60	Qy 1 VQGKGGVWKVIFKTPNQDTEFLERLNLFLEKEGQTVSGMFRALGQEGVSPATVPCISPEL
0,	Matches 283; Conservative 0; Mismatches 0; Indels 0; Gaps
	Match 100.0%;
	; ORGANISM: homo sapiens US-10-037-860-11
	TYPE: PRT
	FastSEQ for
	; NUMBER OF SEO ID NOS: 14
	; PRIOR APPLICATION NUMBER: 09/189,527
	; CURRENT FILING DATE: 2001-01-04
	; CURRENT APPLICATION NUMBER: US/10/037,860
	RENCE: 2581
	TITLE OF INVENTION: ANTRODIFES
	; APPLICANT: Myrna R. Rosenfeld
	; APPLICANT: Josep O. Dalmau
	; APPLICANT: Jerome B. Posner
	GENERAL INFORMATION:
	; Sequence 11, Application US/10037860
	RESULT 1 US-10-037-860-11

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GENERAL INFORMATION:

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APPLICANT: Jorome B. Posner

APPLICANT: Josep O. Dalmau

APPLICANT: Myrna R. Rosenfeld

TITLE OF INVENTION: Ma FAMILY POLYPEPTIDES AND ANTI-Ma

TITLE OF INVENTION: ANTIBODIES

FILE REFERENCE: 2581.1004-004.

CURRENT APPLICATION NUMBER: US/10/037,860

CURRENT FILING DATE: 2001-01-04

PRIOR APPLICATION NUMBER: 09/189,527

PRIOR FILING DATE: 1998-11-10

NUMBER OF SEQ ID NOS: 14

SOFTMARE: FastSEQ for Windows Version 4.0

SEQ ID NO 9

LENCTH: 149

TYPE: PRT

ORGANISM: homo sapiens

US-10-037-860-9
APPLICANT: YUE, Henry
APPLICANT: TANG, Y. Tom
APPLICANT: BAUDMAN, Olga
APPLICANT: BAUDMAN, Olga
APPLICANT: BAUGHN, Mariah R.)
APPLICANT: BAUGHN, Mariah R.)
APPLICANT: LU, Dyung Aina M.
APPLICANT: LU, Dyung Aina M.
APPLICANT: PATTERSON, Chandra
TITLE OF INVENTION: MEMBRANE ASSOCIATED PROTEINS
FILE REFERENCE: PF-0731 USA
CURRENT APPLICATION NUMBER: US/09/965,529
CURRENT APPLICATION NUMBER: 001-05-26
PRIOR APPLICATION NUMBER: 60/164,203; PCT/US00/22315
PRIOR FILING DATE: 1999-08-17; 1999-11-09; 2000-08-14
NUMBER OF SEQ ID NOS: 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 51.6%;
Best Local Similarity 98.7%;
Matches 147; Conservative
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                                                                                                                                                                                                                                                                                                APPLICANT: LAL, Preeti
APPLICANT: YUB, Henry
APPLICANT: TANG, Y. To
APPLICANT: BANDMAN, Ol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 135 DLMHIVQADNPSISVEECLEAFKQVFGSLESRRTAQVRYLKTYQEEGEKVSAYVLRLETL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  195 LRKAVEKRAIPRRIADQVRLEQVMAGATLNQMLWCRLRELKDQGPPPSFLELMKVIREEE
                                                                                                                                                                                                                                                                                                                                                                                                              Application US/09965529
No. US20020182671A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GEKVSAYVLRLETLLRKAVEKRAIPRRIADQVRLEQVMAGATLNQMLMCRLRELKDQGPP 240
                                                                                                                                                                                                                                                                                                                                    in .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 755; DB 13;
Pred. No. 1.8e-58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        194
                                                                                                                                                                                                       LENGTH: 353
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. US20030124649A1 2483172CD1
US-09-969-680A-7
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APPLICANT: TANG, Y. Tom; BANDMAN, Olga
APPLICANT: BURFORD, Neil; AZIMZAI, Yalda
APPLICANT: BURFORD, Neil; AZIMZAI, Yalda
APPLICANT: BAUGHN, Mariah R.; LU, Dyung Aina M.
APPLICANT: PATTERSON, Chandra
TITLE OF INVENTION: MEMBRANE ASSOCIATED PROTEINS
FILE REFERENCE: PF-0731-1 USA
CURRENT APPLICATION NUMBER: US/09/969,680A
CURRENT FILING DATE: 2001-10-02
PRIOR APPLICATION NUMBER: US/07/2315
PRIOR FILING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: 60/149,641
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                                                                                                             Best Loc
Matches
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SEQ ID NO 7
                                                                                                                Query Match
Local Similarity
                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PERL Program SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 7, Application US/09969680A Publication No. US20030124649A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 60/164,203 PRIOR FILING DATE: 1999-11-09
                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR FILING DATE: 1999-08-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc_feat
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 353
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       238 GPPPSFLELMKVIREEEEEEASFENES 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            182 EKVSAYVIRLETILRKAVEKRAIPRRIADQVRLEQVMAGA----TLNQMLWCRLRELKDQ 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       199 RRRLMESLRGPAADVIRILKSNNPAITTAECLKALEQVFGSVESSRDAQIKFLNTYQNPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             122 KRWLAESLRGPALDLMHIVQADNPSISVEECLEAFKQVFGSLESRRTAQVRYLKTYQEEG 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          139 EMLNYILDNVIQPLVESIWYKRLTLFSGRDIPGPGEETFDPWLEHTNEVLEEWQVSDVEK 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             259 EKLSAYVIRLEPLIQKVVEKGAIDKDNVNQARLEQVIAGANHSGAIRRQLWL---TGAGE 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 316 GPAPNLFQLLVQIREEEAKEEEEEAEA 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63 HLIGQAMAHAPQPLL-PMRYRKLRVFSGSAVPAPEEESFEVWLEQATEIVKEWPVTEAEK 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 GKGGVWKVIFKTPNQDTEFLERLNLFLEKEGQTVSGMFRALGQEGVSPATVPCISPELLA 62
                                      GKGGVWKVIFKTPNQDTEFLERLNLFLEKEGQTVSGMFRALGQEGVSPATVPCISPĒLLA 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GKGGVWKVLFKPPTSDAEFLERLHLFLAREGWTVQDVARVLGFQNPTPTP----GPEMPA
               GKGGVWKVLFKPPTSDAEFLERLHLFLAREGWTVQDVARVLGFQNPTPTP---
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                                                                                                             Conservative
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                                                                                                                                  43.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   43.0%; Score 628; DB 9; Length 353; 47.9%; Pred. No. 9e-47; rative 52; Mismatches 75; Indels
                                                                                                             Score 628; DB 10;
Pred. No. 9e-47;
52; Mismatches 75;
                                                                                                                                                            Length 353;
                                                                                                                Indels 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12;
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                                                                                                                Gape
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GENERAL INFORMATION: Sequence 7, App Publication No. Ś

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316 238 259 182 199 문

122 139 63

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Sequence 13, Application US/10037860
Publication No. US20020123114A1
GENERAL INFORMATION:
APPLICANT: Jerome B. Posner
APPLICANT: Josep O. Dalmau
APPLICANT: Myrna R. Rosenfeld
TITLE OF INVENTION: MA FAMILY POLYPEPTIDES ANI
TITLE OF INVENTION: ANTIBODIES:
FILE REFERENCE: 2581.1004-004
CURRENT APPLICATION NUMBER: US/10/037,860
CURRENT FILING DATE: 2001-01-04
PRIOR APPLICATION NUMBER: 09/189,527
PRIOR APPLICATION NUMBER: 09/189,527
PRIOR FILING DATE: 1998-11-10
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; LENGTH: 463
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-037-860-13
Sequence 2385, Application US/10408765A Publication No. US20040101874A1 GENERAL INFORMATION: APPLICANT: Ghosh, Soumitra S.: APPLICANT: Fahy, Eoin D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       142 WT--WAQTLGAAVQPLLEQMLYRELRVFSGNTISIPGALAFDAWLEHTTEMLQMWQVPEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         82 IPGKGGPWEVIVKPRNSDGEFLNRLNRFLEEERRTVSDMNRVLGSDTNCSAPRVTISPEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VQGKGGVWKVIFKTPNQDTEFLERLNLFLEKEGQTVSGMFRALGQEGVSPATVPCISPEL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KRWLAESLRGPALDLMHIYQADNPSISVEECLEAFKQVFGSLESRRTAQVRYLKTYQEEG
                                                                                                                                                                                                                                                                                                                                          AGEKVSSFVLRLEPILQRAVENNVVSRRNVNQTRLKRVLSGATLPDKLRDKLKLMKQRRK 319
                                                                                                                                                                                                                                                                                                                                                                                                 EGEKVSAYVLRLETLLRKAVEKRAIPRRIADQVRLEQVMAGATLNQMLWCRLRELKDQGP 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                     EKRRRLMECLRGPALQVVSGLRASNASITVEECLAALQQVFGPVESHKIAQVKLCKAYQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EKKRWLAESLRGPALDLMHIVQADNPSISVEECLEAFKQVFGSLESRRTAQVRYLKTYQE 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LAHLLGQAMAHAPQPLL-PMRYRKLRVFSGSAVPAPEEESFEVWLEQATEIVKEWPVTEA 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GPAPNLFQLLVQIREEEAKEEEEEAEA 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GPPPSFLELMKVIREEEEEEASFENES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EKVSAYVLRLETLLRKAVEKRAIPRRIADQVRLEQVMAGA----TLNQMLWCRLRELKDQ
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                                                                                                                                                                                                                                                                                         PPSFLBLMKVIREEEEEEASF -- ENESIE 266
                                                                                                                                                                                                                                        PPGFLALVKLLREEEEWEATLGPDRESLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            42.3%; √Score 618.5; DB 13; 50.2%; Pred. No. 9e-46; ative 44; Mismatches 85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           264
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APPLICANT: Taylor, Steven W.
APPLICANT: Glenn, Gary M.
APPLICANT: Glenn, Gary M.
APPLICANT: Warnock, Dale E.
TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
TITLE OF INVENTION: TARGETS FOR THE MITOCHONDRIAL PROTEOME
FILE REFERENCE: 660088.465
FILE REFERENCE: 600088.465
CURRENT APPLICATION NUMBER: US/10/408,765A
CURRENT APPLICATION NUMBER: US/10/408,765A
UNUMBER OF SEQ ID NOS: 3077
NUMBER OF SEQ ID NOS: 3077
SOPTWARE: FRASTSEQ for Windows Version 4.0
SEQ ID NO 2385
                                                                                                                                                                                                                                  APPLICANT: LAL, Preeti.
APPLICANT: YUE, Henry
APPLICANT: TANG, Y. Tom
APPLICANT: BANDMAN, Olga
APPLICANT: BANDMAN, Olga
APPLICANT: BURFORD, Neil
APPLICANT: BURFORD, Neil
APPLICANT: BUTFORD, Neil
APPLICANT: BUTFORD, Mariah R.
APPLICANT: LU, Dyung Aina M.
APPLICANT: LU, Dyung Aina M.
APPLICANT: PATTERSON, Chandra
TITLE OF INVENTION: MEMBRANE ASSOCIATED PROTEINS
FILE REFERENCE: PF-0731 USA
CURRENT APPLICATION NUMBER: US/09/965,529
CURRENT APPLICATION NUMBER: US/09/965,529
PRIOR APPLICATION NUMBER: 60/149,641; 60/164,203; PCT/US00/22315
PRIOR FILING DATE: 1999-08-17; 1999-11-09; 2000-08-14
NUMBER OF SEQ ID NOS: 74
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US-09-965-529-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/09965529 Publication No. US20020182671A1 GENERAL INFORMATION:
                                                                                                                                                           SOFTWARE: PERL Program
SEQ ID NO 1
LENGTH: 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 40.8%; Score 597; DB 16; Best Local Similarity 46.3%; Pred. No. 6.8e-44; Matches 132; Conservative 48; Mismatches 79;
        ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. US20020182671A1 112301CD1
-09-965-529-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 452
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                     TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         115 PVTEAEKKRWLAESLRGPALDLMHIVQADNPSISVEECLEAFKQVFGSLESRRTAQVRYL 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  146 VRSPPL---
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US-09-804-014A-16
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Best Local S
Matches 128
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                                                                                                                                                                                                                                              SOFTWARE: PatentIn Ver.
SEQ ID NO 16
LENGTH: 351
                                                                                                                              Query Match 40.8%; Score 596.5; DB 1
Best Local Similarity 48.3%; Pred. No. 5.3e-44;
Matches 128; Conservative 49; Mismatches 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Fernandes, Elma
APPLICANT: Shimkete, Richard
APPLICANT: Spaderna, Steven
APPLICANT: Wajumder, Kumud
TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoding Same
FILE REFERICE: 15966-721 US
CURRENT APPLICATION NUMBER: US/09/804,014A
CURRENT FILING DATE: 2002-04-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 60/188,316
PRIOR FILING DATE: 2000-03-10
PRIOR APPLICATION NUMBER: 60/188,277
PRIOR FILING DATE: 2000-03-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Li,
APPLICANT: Pac
                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 60/189,140
PRIOR FILING DATE: 2000-03-14
PRIOR APPLICATION NUMBER: 60/190,401
PRIOR FILING DATE: 2000-03-17
                                                                                                                                                                                                                                                                                               PRIOR FILING DATE: 2000-03-17
NUMBER OF SEQ ID NOS: 75
                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 60/189,139
PRIOR FILING DATE: 2000-03-14
                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 60/190,231
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                 61 LAHLLGQAMAHAPQPLLP-MRYRKLRVFSGSAVPAPEEESFEVWLEQATEIVKEWPVTEA 119
                                                                                      1 VQGKGGVWKVIFKTPNQDTEFLERLNLFLEKEGQTVSGMFRALGQEGVSPATVPCISPEL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     h 40.8%; Score 596.5; DB 9; Similarity 48.3%; Pred. No. 5.3e-44; 28; Conservative 49; Mismatches 75;
                                                               IPGKGGIWRVIFKPPDPDNTFLSRLNEFLAGEGMTVGELSRALGHENGSLDPEQGMIPEM
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Sequence 10, Application US/10341434
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Matches
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SEQ ID NO 1
LENGTH: 351
TYPE: PRT
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PRIOR FILING DATE: 1999-11-09
                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
nes 128; Conserv
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APPLICANT: TANG, Y. Tom, BANDMAN, Olga
APPLICANT: BURFORD, Neil; AZIMZAI, Yalda
; APPLICANT: BURFORD, Neil; AZIMZAI, Yalda
; APPLICANT: BURFORD, Neil; AZIMZAI, Yalda
; APPLICANT: BATTERSON, Chandra
TITLE OF INVENTION: MEMBRANE ASSOCIATED PROTEINS
FILE REFERENCE: PF-0731-1 USA
CURRENT APPLICATION NUMBER: US/09/969,680A
CURRENT FILING DATE: 2001-10-02
PRIOR APPLICATION NUMBER: US/09/2315
PRIOR APPLICATION NUMBER: 60/149,641
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens
PARTIRE:
RAMPIKEY: misc feature
OTHER INFORMATION: Incyte ID No. US20030124649A1 112301CD1
                                                                                                                                                                                     180 EGEKVSAYVLRLETLLRKAVEKRAIPRRIADQVRLEQVMAGA---TLNQMLWCRLRELKD 236
                                                                                                                                                                                                                                                                                                                                                                                     142 WAPMLAQAL-EALQPALQCLKYKKLRVFSGRESPEGEBBFGRWMFHTTQMIKAWQVPDV 200
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                                                                                                                                                                                                                                                                                                                                                                                                                              61 LAHLLGQAMAHAPQPLLP-MRYRKLRVFSGSAVPAPEEESFEVWLEQATEIVKEWPVTEA 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       82 IPGKGGIWRVIFKPPDPDNTFLSRLNEFLAGEGMTVGELSRALGHENGSLDPEQGMIPEM 141
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DGPAPGFLQLLVLIKDYEAAEEEEA 340
                                                          QGPPPSFLELMKVIRE---EEEEEA 258
                                                                                                                                                                                                                                                                                        EKKRWLAESLRGPALDLMHIVQADNPSISVEECLEAFKQVFGSLESRRTAQVRXLKTYQE 179
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                                                                                                                           DEEKLSAYVLKLEPLLQKLVQRGAIERDAVNQARLDQVIAGAVHKTIRREL-----NLPE
                                                                                                                                                                                                                                                             EKRRRLLESLRGPALDVIRVLKINNPLITVDECLQALEEVFGVTDNPRELQVKYLTTYQK
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FILE REFERENCE: 2581.1004-004

CURRENT APPLICATION NUMBER: US/10/037,860

CURRENT FILING DATE: 2001-01-04

PRIOR APPLICATION NUMBER: 09/189,527

PRIOR FILING DATE: 1998-11-10

NUMBER OF SEQ ID NOS: 14

SOFTMARE: FASESEQ for Windows Version 4.0

SEQ ID NO 7

LENGTH: 195

TYPE: PRT

ORGANISN: homo sapiens

US-10-037-860-7
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US-10-341-434-10
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                                                                         Query Match
Best Local Similarity
Matches 113; Conserv
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Best Local
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LENGTH: 351
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Jerome B. Posner
APPLICANT: Josep O. Dalmau
APPLICANT: Myrna R. Rosenfeld
TITLE OF INVENTION: MA FAMILY POLYPEPTIDES AND ANTI-MA
TITLE OF INVENTION: ANTIBODIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Origene Technologies
TITLE OF INVENTION: Differentially Regulated Prostate Cancer Genes
FILE REFERENCE: 9U 204 205 R1.
CURRENT APPLICATION NUMBER: US/10/341,434
CURRENT FILING DATE: 2003-07-18
PRIOR APPLICATION NUMBER: US 60/348,164
PRIOR FILING DATE: 2002-01-15.
PRIOR PILING DATE: 2002-01-15.
PRIOR APPLICATION NUMBER: US 60/348,119
PRIOR PILING DATE: 2002-01-15.
PRIOR PILING DATE: 2002-01-15.
PRIOR PILING DATE: 2002-01-15.
PRIOR FILING DATE: 2002-01-15.
PRIOR PILING DATE: 2002-01-15.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   142 WAPMLAQAL-EALQPALQCLKYKKLRVFSGRESPEPGEEEFGRWMFHTTQMIKAWQVPDV 200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        82 IPGKGGIWRVIFKPPDPDNTFLSRLNEFLAGEGMTVGELSRALGHENGSLDPEQGMIPEM
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1 VQKKGGVWKVIFKTPNQDTEFLERLNLFLEKEGQTVSGMFRALGQEGVSPATVPCISFEL
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Similarity 48.3%; Pred. No. 5.3e-44;
28; Conservative 49; Mismatches 75; Indels 13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QGPPPSFLELMKVIRE---EEEEEA 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DEEKLSAYVLRLEPLLOKLVQRGAIERDAVNQARLDQVIAGAVHKTIRREL-----HLPH
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                                                                      40.6%; Score 593; DB 13; ilarity 98.3%; Pred. No. 4.9e-44; Conservative 1; Mismatches 1;
                                                                                                                             Length 195;
                                                                               Gaps
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Sequence 40, Application US/09804014A
Publication No. US20030064489A1
GENERAL INFORMATION:
APPLICANT: Li, Li
APPLICANT: Padigaru, Muralidhara
APPLICANT: Vernet, Corine
APPLICANT: Vernet, Corine
APPLICANT: Shimkete, Richard
APPLICANT: Shimkete, Richard
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US-10-037-860-4
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PRIOR FILING DATE: 1998-11-10
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 38.6%; Score 564; DB 13; Best Local Similarity 47.0%; Pred. No. 3.5e-41; Matches 117; Conservative 47; Mismatches 73;
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APPLICANT: Fernandes, Elma
APPLICANT: Shimkets, Richard
APPLICANT: Shimkets, Richard
APPLICANT: Spaderna, Steven
APPLICANT: Majumder, Kumud
TITLE OF INVENTION: Novel Polypeptides and Nucleic .
FILE REFERENCE: 15966-721 US
CURRENT APPLICATION NUMBER: US/09/804,014A
CURRENT FILING DATE: 2002-04-24
PRIOR APPLICATION NUMBER: 60/188,316
PRIOR FILING DATE: 2000-03-10
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APPLICANT: Josep O. Dalmau
APPLICANT: Myria R. Rosenfeld
TITLE OF INVENTION: Ma FAMILY POLYPEPTIDES AND ANTI-Ma
TITLE OF INVENTION: MATIBODIES
FILE REFERENCE: 2581.1004-004
CURRENT APPLICATION NUMBER: US/10/037,860
CURRENT FILING DATE: 2001-01-04
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 GKGGVWKVIFKTPNODTEFLERLMLFLEKEGQTVSGMFRALGQEGVSPATVPCISPELLA 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EKVSAYVLRLETLLRKAVEKRAIPRRIADQVRLEQVMAGA----TLNQMLWCRLRELKDQ 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RRRLMESLRGPAADVIRILKSNNPAITTAECLKALEQVFGSVESSRDAQIKFLNTYQNPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GPPPSFLEL 246
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                                                                                                                 Acids Encoding
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US-09-804-014A-39
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                                                                                                     CURRENT APPLICATION NUMBER: US/09/804,014A
CURRENT FILING DATE: 2002-04-24
PRIOR APPLICATION NUMBER: 60/188,316
PRIOR FILING DATE: 2000-03-10
PRIOR APPLICATION NUMBER: 60/188,277
PRIOR FILING DATE: 2000-03-10
PRIOR APPLICATION NUMBER: 60/189,139
PRIOR APPLICATION NUMBER: 60/189,139
PRIOR FILING DATE: 2000-03-14
PRIOR FILING DATE: 2000-03-14
PRIOR APPLICATION NUMBER: 60/189,140
PRIOR APPLICATION NUMBER: 60/190,401
PRIOR FILING DATE: 2000-03-17
PRIOR FILING DATE: 2000-03-17
PRIOR FILING DATE: 2000-03-17
PRIOR FILING DATE: 2000-03-17
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APPLICANT: Pad
APPLICANT: Ver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 39, Application US/09804014A Publication No. US20030064489A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 40
LENGTH: 318
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Best Local Similarity
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PRIOR FILING DATE: 2000-03-14
PRIOR APPLICATION NUMBER: 60/190,401
PRIOR FILING DATE: 2000-03-17
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NUMBER OF SEQ ID NOS: 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoding FILE REFERENCE: 15966-721 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
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NAME/KEY: VARIANT
LOCATION: (20)
OTHER INFORMATION: Wherein Kaa is any amino acid as defined in
OTHER INFORMATION: specification
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ORGANISM: Homo sapiens
                                   APPLICATION NUMBER: 60/190,231 FILING DATE: 2000-03-17
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SEQ ID NOS:
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Shimkets, Richard;
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; Pred. No. 4.6e-41.
45; Mismatches 6
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RESULT 15
US-09-804-014A-73
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CURRENT APPLICATION NUMBER: US/09/804,014A
CURRENT FILING DATE: 2002-04-24
PRIOR APPLICATION NUMBER: 60/188,316
PRIOR FILING DATE: 2000-03-10
PRIOR FILING DATE: 2000-03-10
PRIOR PILING DATE: 2000-03-10
PRIOR PILING DATE: 2000-03-10
PRIOR PILING DATE: 2000-03-14
PRIOR FILING DATE: 2000-03-14
PRIOR FILING DATE: 2000-03-14
PRIOR FILING DATE: 2000-03-14
PRIOR APPLICATION NUMBER: 60/189,140
PRIOR APPLICATION NUMBER: 60/190,401
PRIOR APPLICATION NUMBER: 60/190,401
PRIOR APPLICATION NUMBER: 60/190,401
PRIOR PILING DATE: 2000-03-17
PRIOR FILING DATE: 2000-03-17
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                                                                                     US-09-804-014A-73
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APPLICANT: Li, Li
APPLICANT: Padigaru,
APPLICANT: Vernet,
Ouery Match DB 10;
Best Local Similarity 50.9%; Pred. No. 5.6e-40;
Matches 113; Conservative 41; Mismatches 66;
                                                                                                                                                                          NUMBER OF SEQ ID NOS: 75
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Ver.
SEQ ID NO 39
LENGTH: 321
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TITLE OF INVENTION: Novel Polypeptides and Nucleic
FILE REFERENCE: 15966-721 US
                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 60/190,231 PRIOR FILING DATE: 2000-03-17
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TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                        TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                     ENGTH:
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Local Similarity 48.6%; Pred. No. 7.7e-41;
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Shimkets, Richard
Spaderna, Steven
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1 VQGKGGVWKVIFKTPNQDTEFLERLNLFLEKEGQTVSGMFRALGQEGVSPATVPCISPEL

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Title:
Perfect score:
Sequence:
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Maximum DB
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No.
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Maximum Match 100%
Listing first 45 summaries
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length: 2000000000
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Match
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2423
1 MPLTLLQDWCRGEHLNTRRC.....VESGNGNWAWDKSHPKSKAK 463
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1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*

2: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

3: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/pcTUS_COMB.pep:*

6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*
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(c) 1993 - 2005 Compugen Ltd
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US-09-949-016-8626
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US-09-92-940-11866
US-09-902-540-11866
US-09-902-911848
US-09-903-911848
US-09-9190-911848
US-09-9189-110-5058
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US-09-918-09-1259
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US-09-918-09-1259
US-08-466-390-2
US-08-470-950-2
US-08-470-950-2
US-08-470-950-2
US-08-486-390-2
US-08-486-390-2
US-08-483-924-2
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US-09-189-527-4
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Sequence 2, Appli
Sequence 8626, Ap
Sequence 20182, Appl
Sequence 3163, Appl
Sequence 32743, A
Sequence 11866, A
Sequence 11866, A
Sequence 11846, A
Sequence 3259, Ap
Sequence 2259, Ap
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Sequence 26726, A
Sequence 2798, A
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US-09-189-527-13
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Best Local
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<b>4</b> .	44	43	42	41	40	39	38	37	36	35	34	u u	32	31	30	29	28
96.5	96.5	96.5	96.5	96.5	96.5	97	97	97	97	97	97	97.5	97.5	97.5	98	98.5	98.5
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US-09-252-991A-28918	US-09-252-991A-17953	US-09-913-301-2	US-09-913-301-5	US-09-252-991A-20455	US-09-252-991A-24973	US-09-252-991A-31502	US-07-945-283-2	US-09-107-433-3227	US-09-252-991A-30867	US-09-583-110-3291	US-09-252-991A-26482	US-09-431-184A-4	US-08-841-349-4	US-09-252-991A-28446	US-09-902-540-13635	US-09-252-991A-23346	US-09-489-039A-12568
Sequence 28918, A	Sequence 17953, A	Sequence 2, Appli	Sequence 5, Appli	Sequence 20455, A	Sequence 24973, A	Sequence 31502, A	Sequence 2, Appli	Sequence 3227, Ap	Sequence 30867, A	Sequence 3291, Ap	Sequence 26482, A	Sequence 4, Appli	Sequence 4, Appli	Sequence 28446, A	Sequence 13635, A	Sequence 23346, A	Sequence 12568, A

## ALIGNMENTS

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FILE REFERENCE: SLK98-01
CURRENT APPLICATION NUMBER: US/09/189,527A
CURRENT FILING DATE: 1998-11-10
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PastSEQ for Windows Version 3.0
SEQ ID NO 13
LENGTH: 462
TYPE: PRT
ORGANISM: homo sapiens
US-09-189-527-13
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GENERAL INFORMATION:
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APPLICANT: Josep O. Dalmau
APPLICANT: Myrna R. Rosenfeld
TITLE OF INVENTION: Ma Family Polypeptides and Anti-Ma
TITLE OF INVENTION: Antibodies
                                                                                                                                                                                                                                                                                                                                        LELAQDIDYALLPREIPGKGGPWEVIVKPRNSDGEFLNRLNRFLEEERRTVSDMVRVLGS
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LRDKLKLMKQRRKPPGFLALVKLLREEEEWEATIGPDRESLEGLEVAPRPPARITGVGAV
                                                             KIAQVKLCKAYQEAGEKVSSFVLRLEPLLQRAVENNVVSRRNVNQTRLKRVLSGATLPDK
                                                                                   KIAQVKLCKAYQEAGEKVSSFVLRLEPLLQRAVENNVVSRRNVNQTRLKRVLSGATLPDK
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100.0%; Pred. No. 4
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Sequence 7, Application US/09189527A
Patent No. 6387639
GENERAL INFORMATION:
APPLICANT: Josep O. Dalmau
APPLICANT: JOSep O. Dalmau
APPLICANT: Myrna R. Rosenfeld
TITLE OF INVENTION: Ma Family Polypeptides and
TITLE OF INVENTION: Antibodies
FILE REFERENCE: SLK98-01
CURRENT APPLICATION NUMBER: US/09/189,527A
CURRENT FILING DATE: 1998-11-10
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSEQ for Windows Version 3.0
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CURRENT FILLING DATE: 1998-11-10
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 4
LENGTH: 329
TYPE: PRT
ORGANISM: homo sapiens
US-09-189-527-4
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TITLE OF INVENTION: Antibodies

TITLE OF REFERENCE: SLK98-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 31.6%; Score 766.5; DB 3; Best Local Similarity 50.2%; .Pred. No. 4.1e-73; Matches 157; Conservative 50; Mismatches 103;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Solimena, Michele
ITITLE OF INVENTION: INTERACTING POLYPEPTIDES FOR
ITITLE OF INVENTION: AUTOANTIGENS OF AUTOIMMUNE DISE
FILE REFERENCE: 101918-200 (OCR-941)
CURRENT APPLICATION NUMBER: US/09/368,590
CURRENT FILING DATE: 1999-08-04
EARLLER APPLICATION NUMBER: 60/095,657
EARLLER FILING DATE: 1998-08-07
NUMBER OF SEQ ID NOS: 8
SOFTMARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 7
LENGTH: 195
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Patent No. 6187563
                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity Matches 100; Conserv
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                                                                                                                                                                                                                                                                                                              106 LNRFLEEERRTVSDMNRVLGSDTNCSAPRVTISPEFWTWAQTLGAAVQPLLEQMLYRE--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62 AQAILLELAQDIDYALLPREIPGKGGPWEVIVKPRNSDGEFLNRLNRFLEEERRTVSDMN 121
                                                                                                                                                                                                                                                                                                                                                                                            60 ENAQAILLELAQDIDYALLPREIPGK------GGPWEVIVKPRNSDGEFL---NR 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 ANAVLLELLEDTDVSAIPSEVQGKGGVWKVIFKTPNQDTEFLERLNLFLEKEGQTVSGMF
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93; Conserv
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                                                                                                                   QLFLRDLRQALVVLRNQEMALSGAELPGTVESVEEALKQHRDFLTTMELSQQKMQVAVQA 959
                                                                                                                                                                                                                                     -LRVFSGN--TISIPGA-----LAFDAWLEHTT----EMLQMWQVPEGEKRRRLMEC---
      ATLPDKL----RDKLKLMKQRRKPPGFLALVKLLREEEEWEATL---GPDRESLE-
                                        AEGLLRQGNIYGEQAQEAVTR---LLEKNQENQLRAQQWMQKLHDQLELQHFLRDCHELD 1016
                                                                                                                                                        ---LRG--PALQVVSG--LRASNASI--TVEECLAALQQVFGPVESHKIAQVKLCKAYQE
                                                                                                                                                                                                                                                                          LORFLHDLDAFLDWLVRAQEAAGGSEGP----LPNSLEEADALLARHAALKEEVDQREED
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                                                                                                                                                                                                                                                                                                                                                                                                                                               5.0%; Score 122; DB 3; Length 2293; 25.1%; Pred. No. 0.0096;
                                                                               -GEKVSSFVLRLEPLLQRAVENNVVSRRNV----NQTRLKRVLS-----G
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                                                                                                                                                                                                                                                                                                                                                                                                                                57; Mismatches 144;
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259 899 208 163 787

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CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
SEQ ID NO 8626
SEGTMARE: FRASESEQ for Windows Version 4.0
SEQ ID NO 8626
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US-09-949-016-8626
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                                                                                      US-09-252-991A-20182
Sequence 20182, Application US/09252991A
PATENT NO. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AN
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ORGANISM: Human
-09-949-016-8626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: CL001307
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                                                                                                                                                          560
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                                                                                                                                                          LAEIFCQTGGVEDQEEWHAQVVEELSNFKSQKV 592
                                                                                                                                                                                             LVKL-----LREEEEWEATLGPDRESLEGLEV 352
                                                                                                                                                                                                                              ROQVENRVVEEAKGLLDKVKDGGYRP--AEDKIFPVPEEPPVKKLMRTSTPPPASVINNM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRVTISPEFWTWAQTLGAAVQPLLEQMLYRELRVFSGNTISIPGALAFDAWLEHTTEMLQ
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   SEQUENCES RELATING
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       118
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Sequence 53, Application US/09919497

Patent No. 6773883

GENERAL INFORMATION:

APPLICANT: Mutter, George L.

TITLE OF INVENTION: PROGNOSTIC CLASSIFICATION OF FILE REFERENCE: B0801/7225

CURRENT APPLICATION NUMBER: US/09/919,497

CURRENT FILING DATE: 2001-07-31

PRIOR FILING DATE: 2000-07-31
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CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR PELICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 20182
LENGTH: 341
TYPE: PRI
                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Homo sapiens US-09-919-497-53
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SOPTWARE: Patentin version 3.0
SEQ ID NO 53
LENGTH: 373
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                               Local Similarity
mes 97; Conserv
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les 66; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   123 HRPALROPRHRRLPP---AVPRRDLRPDHGQPRAGPARRGLRRGHRGGLRAARFRLHFPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  208 CLRGPALQVVSGLRASNASITVEECLAALQQVFGPVESHKIAQVKLCKA------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       68 PPAQPYHSSHRPHRGRPALPAALRADPRLRRGSRGR--SQRRPCPTRRQ---AEAAFDDR 122
                                                  80 VQF-VLRRTGPSLAGRPSSDSCPPPERCLIRASLPVKPRAALG------CEPRKTL
                                                                                                    73 IDYALLPREIPGKGG-----PWE-----VIVKPRNSDGEFLNRLNRFLESERRTV 117
                                                                                                                                                        20 VVCGVSEQTTCQEVVIALAQAIGQTGRFVLVQRLREKERQLLPQECPVGAQATCGQFASD
                                                                                                                                                                                                        22 LILGIPEDCGEDEFEETLQEACRHLGRYRVIGRMFRREE-----NAQAILLELAQD
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SDMNRVLGSDTNCSAPRVTISPEFWTWAQTLGAAVQPLLEQMLYRELRVFSGNTISIPGA 177
                                                                                                                                                                                                                                                             4.5%; Score 110; DB 4; ilarity 24.2%; Pred. No. 0.0092; Conservative 49; Mismatches 144
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US-09-949-016-11663
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PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 11663
LENGTH: 384
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Best Local
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307

CURRENT FAPPLICATION NUMBER: U$/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR PILING DATE: 2000-10-26*

PRIOR PILING DATE: 2000-10-3

PRIOR FILING DATE: 2000-10-3

PRIOR FILING DATE: 2000-10-3

PRIOR FILING DATE: 2000-10-3
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97; Conserv
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                                                                                                                                                                                                          LAFDAWLEHTTEMLQMWQVPEGEKRRRLMECLRGPALQVVSGLRASNA---SITVEECLA 234
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                                                                                                                                                                                                                                                                                                                     VQF-VLRRTGPSLAGRPSSDSCPPPERCLIRASLPVKPRAALG-----CEPRKTL 139
                                                                                                                                                                                                                                                                                                                                                     IDYALLPREIPGKGG-----PWE-----VIVKPRNSDGEFLNRLNRFLEEERRTV
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                                                                                                                               ALQQVFGP-------VESHKIAQVK----LCKAYQEAGEKVSSFVLRLEPL 274
                                                                                                                                                                      EAF--W----EQELRREQAREREGQARL-QALSAATAEHAARLQALDAQARALEAELQLA
                                                                                                                                                                                                                                                                                SDMNRVLGSDTNCSAPRVTISPEFWTWAQTLGAAVQPLLEQMLYRELRVFSGNTISIPGA 177
                         AQELEELN --- RELROCNLOQFIQQTGAALPPPPRPD---
                                                           LORAVENNVVSRRNVNOTRLKRVL--SGATLPDKLRDKLKLMKORRKPPGFLALVKLLRE 332
                                                                                            A--EAPGPPSPMASATERLEQDIAVQERQSAEVQGSLALVSRALEAAERA-----LQAQ 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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24.2%;
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Sequence 14780, Application US/09902540

Patent No. 6833447

GENERAL INFORMATION:
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
APPLICANT: Wiegand, Roger C.
FITLE OF INVENTION: Myxococcus xanthus Genome Seq.
FILE REFERENCE: 38-10(15849)B
CURRENT APPLICATION UMMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                   347
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CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 32743
LENGTH: 718
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                              394 RGGVARAGSRGSRK-----RKRHTFCYSCGEDGHIRVQCINPSNLLL------VKQK 439
                                                                                                                                                                                                                                                                                                                                                                                                       179 DGHRRCLHPRLPAGRRGLPRRRLRGAV--ANLPSRARDH----GVRRRPAGGGLFRLGLA 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        122 PEKPHHVERPRHVDAYRQPGQRATR---RLSPRPGPRRRRTDRHAGGGGPRQRALHLARA 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      242 PVESHKIAQVKLCKAYQEAGEKVSSFVLRLEPL-------LQRAVE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----NNVVSRRNVNQTRLKRVLSGATLPDKLRDKLKLMKQRRKPPG----FLALV 327
                                                                                                                                                                                                                                                                       QRTVPGDAARTRPAADRRDRRLRRRRAPPARGRTGRGGGGRQPRLPAGAIPQPA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----ESLLGAPSESHAGAQPRPRGGPHDAELLEVAAAPAP 372
                                                                                                                                -GEPPQGWLQRRPRCPPAFPPRSAGGGARGHLRGLHRRPAPVRRRARPRGSQRKRVAAGG
                                                                                                                                                                                                                                                                                                                                  KLLREEEEWEATLGPDRESLEGLEVAPRPPAR-ITG-----
RGGPGRAGLPAHRRRHFGLPRRRHSYRPA---DGH-RAGLPGPRSQYLQGAPGDPAVRHR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 110; DB 4; Length 718; Pred. No. 0.027; 1; Mismatches 93; Indels 1
                                                                                                                                                                                                  -----RGOHR------
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Sequences

and Uses Thereof

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Myxococcus xanthus US-09-902-540-14780
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PRIOR FILING DATE: 2001-07-10:
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 11866
LENGTH: 312
TYPE: DET
                                                                                                                                                                  Query Match
Best Local S
Matches 67
                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:

APPLICANT: Goldman, Barry S.

APPLICANT: Hinkle, Gregory J.

APPLICANT: Slater, Steven C.

APPLICANT: Wiegand, Roger C.

APPLICANT: Wiegand, Roger C.

TITLE OF INVENTION: Myxococcus xanthus Genome
FILE REFERENCE: 38-10(15849)B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 11866, Application US/09902540 Patent No. 6833447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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Best Local Similarity
                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/902,540 CURRENT FILING DATE: 2001-07-10
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TYPE: PRT
                                                                                                                                                                Local Similarity
nes 67; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              441 QLEAWK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                346 SLEGLEVAPRPPARITGVGAVPLP----ASGNSFDARPSQGYRRRRGRGQHRR 394
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LDIESRTYAAMEG-AVEDLPRCAPARLLEETFRLIRGG-VSAPALKULDA-----LDALK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ISPEFWTWAQTLGAAVQPLLE---- OMLYRELRVFSGNTISIPGALAFDAWLEHTTEMLQ 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LLPREIPGKGGPWEVIVKPRNSDGEFLNRLNRFLEEERRTVSDMNRVLGSDTNCSAPRVT 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GEDEGDGEDLLITHDNVFGTAQQDAR------RRDFTINGLFYDVAEGRVIDY-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GEDEFE-----ETLQEACRHLGRYRVIGRMFRREENAQAILLELAQD--IDYA 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ILLPPVNAYLKOHGKEGEKTFYAFAESLDRR------VSAGEALDDAILLAMLL 350
                                                                                                                                ITVEECLAALQQ--VFGEVESHKIAQVKLCKAYQEA------GEKVSSFVLRLEPL 274
 GFLALVKLLREESEWEATIGPDRESLEGLEVAPRPPARITGVGAVPLPASGNSFDARP--
                                                                 LQRAVB-NNVVSRRNVNQTRLKRVLSGATLPDK----LRDKLKLMKQRR------KPP 321
                                                                                                  IELERSLDAMDHFAVLGLKPGAPASEVK--QAYYNASRRFHPDRYFGKNLGSFRARMERI
                                 Conservative
                                                                                                                                                                  4.3%; Score 104; DB. Conservative 30; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4.3%; Score 104.5; DB
24.0%; Pred. No. 0.058;
ative 45; Mismatches 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----ERRRSAAFKRHPLFSEALTVFEMTVEAT-GENRE
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                                                                                                                                                                                                     DB 4;
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                                                                                                                                                                       84;
                                                                                                                                                                                                   Length 312;
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                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                            and Uses Thereof
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US-09-949-016-7309 RESULT 13

Sequence 7309, Application US/09949016

Patent No. 6812339

Patent No. 6812339

PATENT INFORMATION:
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
APPLICAT: VENTER, J. Craig et al.
APPLICATION: WITH HUMAN DISEASE, METHODS OF DETECTION AND TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND FILLE REFERENCE: CLO01307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

DRIOR FILING DATE: 7000-10-00

DRIOR APPLICATION NUMBER: 60/237,768

USES

THEREOF

FILING DATE: 2000-10
APPLICATION NUMBER:

2000-10-03

60/231,498

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PRIOR FILING DATE: 199-01-29

NUMBER OF SEQ ID NOS: 14342

SEQ ID NO 11848

TYPE: PRT

PRIOR FILING DATE: 1990-01-29

NUMBER OF SEQ ID NOS: 14342

SEQ ID NO 11848

LENGTH: 383

TYPE: PRT
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APPLICANT: Gary Br
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                                                                                                                                                                                                                                                                                                                                                                                                  Matches 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: GARY Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                / Match 4.3%; Score 104; DB 4 Local Similarity 22.5%; Pred. No. 0.042; Pres 60; Conservative 44; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           116 PSAPAQHLLTPEP-----PPVHQLSSPPPAPRPPVASSGPSSIPPP-
                                       347
                                                                            238 NKSRLVAEHFDWCHTVDRLKIATRLNEOR---PAHLPPLKVLIQINISDEQSKSGIPLEA
                                                                                                                                                           198
                                                                                                                                                                                                                                       165
                                                                                                                                                                                                                                                                          174 IPGALAFDAWLEHTTEMLQMWQVPEGEKRRLMECLRGPALQVVSGLRASNASITVEBCL 233
                                                                                                                                                                                                                                                                                                                                                         114 RRTVSDMARVLGSDTNCSAPRVTISPEFWTWAQTLGAAVQPLLEQMLYRELRVFSGNTIS 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 162 PPPDDGASEARRAERQARLARHPYLARTGRLAELIARGKAAIASGDWERAYHDF-----
    295
                                                                                                         290 NQTRL-KRVLSGATLPDKLRDKLKLMKQRRKPPGFLALVKLLRE--EEEWEATLGPDRES 346
                                                                                                                                                                                                234
                                                                                                                                                                                          AALQQVFGPVESHKIAQVKLCKAYQEAGEKVSSFVLRLEPLLQRA----VENNVVSRRNV 289
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                                                                                                                                                           AAGORAFG--ENY-----VOEGVEKINHF------QQAGVSGLQWHFIGPLQS
                                                                                                                                                                                                                                                                                                                      QRGAAELHR-CRSETLCFTLRATISSSFITHPRNMNDIAHNLAQ---VRD------K 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --H-QVQTMDPKNREVALLLVKARRGHDSQRATIEVARG 251
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                                     LEGL--EVAPRPPARITGVGAVPLPAS 371
                                                                                                                                                                                                                                     ISGAAA-----RCGRAPEEVTLLAVSKTKPASAIEEAI 197
    LDĞLAAETAELPHLELRĞLMATPAPES 321
                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 4; Length 383;
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FILE REFERENCE: PATHO0-07A
CURRENT APPLICATION NUMBER: US/09/583,110
CURRENT FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/107,433
PRIOR APPLICATION NUMBER: US 60/085,131
PRIOR FILING DATE: 1998-06-30
PRIOR FILING DATE: 1998-05-12
PRIOR PAILING DATE: 1998-05-12
PRIOR APPLICATION NUMBER: US 60/051,553
PRIOR APPLICATION NUMBER: US 60/051,553
PRIOR FILING DATE: 1997-07-02
NUMBER OF SEQ ID NOS: 5322
SEQ ID NO 5058
SEQ ID NO 5058
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US-09-949-016-7309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 5058, Application US/09583110 Patent No. 6699703 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 7309
LENGTH: 2600
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Best Local :
                                                                                                                                                                   TYPE: PRT
ORGANISM: Streptococcus pneumoniae
-09-583-110-5058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Lynn Doucette-Stamm et al.
TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         / Match 4.3%; Score 104; DB 4; Length 2600; Local Similarity 23.3%; Pred. No. 1; hes 84; Conservative 52; Mismatches 125; Indels 100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1400 B 1400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1238 QLFLRDLRQALVVLRNQEMALSGAELPGTVESVEEALKOHRDFLTTMELSQQKMQVAVQA 1297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1182 YARIVAASEALLAADGABLGPGLALDEWLPHLELGWHKLLGLWEA----RREALVQAHIY 1237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1071 EPRQAALLEEA-----ALLAERFPAQAARLHQGAEELGAEWGALASAAQACGEAVAAAGR 1125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       164 -LRVFSGN--TISIPGA-----LAFDAWLEHTT----EMLQMWQVPEGEKRRLMEC---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     209 ---LRG--PALQVVSG--LRASNASI--TVEECLAALQQVFGPVESHKIAQVKLCKAYQE
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                                      31 GEDEFEETLQEA--CRHLGRYRV--IGRMFRREENAQAILL----ELAQDIDYALLPREI
                                                                                 1 Similarity
91, Conserv
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                                                                                   4.3%;
larity 21.5%;
Conservative 63
                                                                                 Score 103; DB 4; Length 551; Pred. No. 0.098; 63; Mismatches 163; Indels 1
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                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PAGENCY INFORMATION:
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS;
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A;
CURRENT FILLING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR PILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
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PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 32259
LENGTH: 1201
                                                                                                                                                                                                                                                                                                                                                                                      Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               83
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                                                                                   MWQVPEGEKRRLMECLRGPALQV-----
                                                                                                                            PGKGGPWEVIVKPRNSDGEFLNRLNRFLEEE------RRTVSDMNRVLGSDTNCSA 132
                                                                                                                                                                                                                                                                                                  ETLEQALAQRGALDDGESLISRDGYWVGRHFLRVRRSDEAQGGMIARAQELE-ALQERRE 703
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QTRLKRVLSGA-TLPDKL------RDKLKLMKQRRKPPGFLALVKLLRE 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NLF---EMIRLATVNLADIKSSLOPKIYAEMMTVRLAEIKPEPALSGAVENEIATLRO-E 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QVFGPVESHKIAQVKLCKAYQEAGEKV--SSFVLRL----EPLLQRAVENNVVSRRNVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QQDVPKALSCLNLLFDNGKSMTRFVTDLLHYLRDLLIVQTGGENTHHSSVFVENLALPQK
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-VSGLRASNASITVEECLAALQQVFGPVESHKIAQVKLCKAYQEAGEKVSSFVLRLEPLL
                                        LEQEQLSEARLTLQEALDSMALDTERRETLLAERDALRERLDRIRQDARTHKDHAHQLAV 840
                                                                                                                                                                PRVTISPEFWTWAQTLGAAVQPLLEQMLYRELRVFSGNTISIPGALAFDAWLEHTTEMLQ 192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PGKGGPWEVIVKPRNSDGEFLNRLNRFLEEERRT---VSDMNRVLGSDTNCSAPR-VTIS 138
                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                 4.2%; Score 101.5; DB 4; 20.7%; Pred. No. 0.52; tive 58; Mismatches 155;
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                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1201;
                                                                                                                                                                                                                                                                                                                                                                                   Indels 163;
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Result
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1: /cgn2 6/ptodata/1/pubpaa/US07 PUBCOMB.pep:*

2: /cgn2 6/ptodata/1/pubpaa/US06 NEW PUB.pep:*

3: /cgn2 6/ptodata/1/pubpaa/US06 NEW PUB.pep:*

4: /cgn2 6/ptodata/1/pubpaa/US06 PUBCOMB.pep:*

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12: /cgn2 6/ptodata/1/pubpaa/US09 PUBCOMB.pep:*

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Copyright (c) 1993 - 2005 Compugen Ltd.
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10 US-09-804-014A-16

10 US-09-969-680A-1

11 US-10-341-434-10

12 US-10-341-434-1978

13 US-10-094-749-1978

14 US-09-804-014A-3

10 US-09-804-014A-3

10 US-09-804-014A-73
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Sequence 13, Appl
Sequence 2385, App
Sequence 7, Appli
Sequence 7, Appli
Sequence 1, Appli
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Sequence 1978, Ap
Sequence 4, Appli
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Sequence 3, Appl
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37-963-117	7-963-12261	-10-437-963-146	-10-437-963-12262	-437-963-14631	37-963-19907	-10-437-963-122	-10-437-963-12266	0-437-963-11729	4-780A-1	37-963	0-437-963-18572	-10-221-278	-10-291-172	-10-437-963-12258	-963	-10-437-963-11068	-10-374-780	-10-437-963	4-780	S-10-408-765	09-864-761-	-10-029-	-10.	014A-	9-804-014A-	-10-296-115	0-959-539-	-10-094-466-3	-10-037-860-	-10-037-8	US-09-804-014A-74
ø	Ф	ø	Sequence 122620,	æ	ø	æ	æ	e 117296	e 1(	ø	e 1857	equence 35	equence 355,	e 12258	O	e 110685,		185722	equence 1037,	e 299	w	equence 33747,	equence	41, App	e 42	e 12	e 26	e J	e 7,	e 11	Sequence 74, Appl

### ALIGNMENTS

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RESULT 1
US-10-037-860-13
; Sequence 13, Application US/10037860
; Publication No. US20020123114A1
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                          ; TYPE: PRT ; ORGANISM: homo sapiens US-10-037-860-13
                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13
                                                                                                                                                                                                         Ouery Match 100.0%; Score 2423; DB 13; Length 463; Best Local Similarity 100.0%; Pred. No. 2.4e-210; Matches 463; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Jerome B. Posner
APPLICANT: Josep O. Dalmau
APPLICANT: Myrna R. Rosenfeld
TITLE OF INVENTION: MA FAMILY POLYPEPTIDES AND ANTI-MA
TITLE OF INVENTION: ANTIBODIES
FILE REFERENCE: 2581.1004-004
CURRENT FILING DATE: 2001-01-04
PRIOR APPLICATION NUMBER: US/10/037,860
CURRENT FILING DATE: 2001-01-04
PRIOR APPLICATION NUMBER: 09/189,527
PRIOR FILING DATE: 1998-11-10
                                                                                                                                                                                                                                                                                                                                                         LENGTH: 463
121 NRVLGSDTNCSAPRVTISPEFWTWAQTLGAAVQPLLEQMLYRELRVFSGNTISIPGALAF 180
                                       <u>,</u>
                                                                                                                                                                                                           Gaps
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740.5

356

406

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Sequence 2385, Application US/10408765A

Publication No. US20040101874A1

GENERAL INFORMATION:
APPLICANT: Ghosh, Soumitra S.
APPLICANT: Faby, Eoin D.
APPLICANT: Gibson, Bradford W.
APPLICANT: Glenn, Gary M.
APPLICANT: Taylor, Steven W.
APPLICANT: Marnock, Dale E.
APPLICANT: Warnock, Dale E.
TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOM
FILE REFERENCE: 660088.465
CURRENT FILING DATE: 2003-04-04
AUMHER OF SEQ ID NOS: 3077
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 2385
LENGTH: 452
TYPE: PRT
ORGANISM: Homo Sapiens
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 240
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                                                                                                                                                                                 121 NRVIGSDTNCSAPRVTISPEFWTWAQTLGAAVQPLLEQMLYRELRVFSGNTISIPGALAF
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                                                                                                                                                                                                                                                                                                                                                                  h 36.5%; Score 883.5; DB 16; Length 452; Similarity 42.6%; Pred. No. 5.6e-71; O1; Conservative 75; Mismatches 155; Indels 41;
                                                                    GPVESHKIAQVKLCKAYQBAGEKVSSFVLRLEPLLQRAVENNVVSRRNVNQTRI.KRVI.SG
                                                                                                                                                                                                                                         NAQAILLELAQDIDYALLEREIPGKGGPWEVIVKPRNSDGEFLNRLNRFLEEERRTVSDM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GHIRVQCINPSNLLLLVKQKKQAAVESGNGNWAWDKSHPKSKAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GHIRVQCINPSNLLLVKQKKQAAVESGNGNWAWDKSHPKSKAK 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGVGAVPLPASGNSFDARPSQGYRRRRGRGQHRRGGVARAGSRGSRKRKRHTFCYSCGED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GPVESHKIAQVKLCKAY;£AGEKVSSFVLRLEPLLQRAVENNVVSRRNVNQTRLKRVLSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DAWLEHTTEMLOMWQVPEGEKRRRLMECLRGPALQVVSGLRASNASITVEECLAALQQVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DAWLEHTTEMLOMWQVPEGEKRRRLMECLRGPALQVVSGLRASNASITVEECLAALOQVF
                                                                                                                                                ARALGC --- CSLPAESLDAE -- VMPQVRSPPLEPPKESMWYRKLKVFSGTASPSPGEETF
                                                                                                                                                                                                                      NAKAVFIELADTVNYTTLPSHIPGKGGSWEVVVKPRNPDDEFLSRLNYFLKDEGRSMTDV
                                                                                                                                                                                                                                                                                        TGVGAVPLPASGNSFDARPSQGYRRRRGRGQHRRGGVARAGSRGSRKRKRHTFCYSCGED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATLPDKLRDKLKLMKQRRKPPGFLALVKLLREEBEWEATLGPDRESLEGLEVAPRPPARI
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GDKEDFRASQFRFLQTSPKIGEKVSTFLLRLEPLLQKAVHKSPLSVRSTDMIRLKHLLAR
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APPLICANT: LAL, Preeti
APPLICANT: TYUE, Henry
APPLICANT: TANG, Y. Tom
APPLICANT: BANDMAN, Olga
APPLICANT: BANDMAN, Olga
APPLICANT: BANDMAN, Olga
APPLICANT: BANDMAN, Olga
APPLICANT: LU, Dyung Aina M.
APPLICANT: LU, Dyung Aina M.
APPLICANT: LU, Dyung Aina M.
APPLICANT: PATTERSON, Chandra
ITITLE OF INVENTION: MEMBRANE ASSOCIATED PROTEINS
ITITLE OF INVENTION NUMBER: US/09/965,529
CURRENT APPLICATION NUMBER: US/09/965,529
CURRENT FILING DATE: 1999-08-17; 1999-11-09; 2000-08-14
NUMBER OF SEG ID NOS: 74
SOFTWARE: PERL Program
SEC ID NO 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20020182671A1 2483172CD1
US-09-965-529-7
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US-09-965-529-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 33.8%; Score 818; DB 9; Length 353; Best Local Similarity 49.6%; Pred. No. 3.3e-65; Matches 172; Conservative 52; Mismatches 113; Indels 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 7, Application US/09965529 Publication No. US20020182671A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 353
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                 178
                                                                                                                                                                                                    181
                                                                                                                                                                                                                                   110 ARVLGFQNPTPTPGPEMPAEMLNY--ILDNVIQPLVESIWYKRLTLFSGRDIPGPGEETF
                                                                                                                                                                                                                                                           121 NRVLGSDTNCSAPRVTISPEFWTWAQTLGAAVQPLLEQMLYRELRVFSGNTISIPGALAF 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               301 ATLPDKLRDKLKLMKQRRKPPGFLALVKLLREEEEWEAT----LGPDRESLEGLEVAPRP
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                                                                                                                                                                                                                                                                                                             1 MPLTLLQDWCRGEHLNTRRCMLILGIPEDCGEDEFEETLQEACRHLGRYRVIGRMFRREE
                                                                                                                                                                                                                                                                                                                                                                                       1 MAMTLLEDWCRGMDVNSQRALLVWGIPVNCDEAEIEETLQAAMPQVS-YRMLGRMFWREE 59
                                                                                                                                                             DAWLEHTTEMLOMWQVPEGEKRRIMECLRGPALQVVSGLRASNASITVEECLAALQQVF
                                                                                                             GPVESHKIAQVKLCKAYQEAGEKVSSFVLRLEPLLQRAVENNVVSRRNVNQTRLKRVLSG
                   ANHSGAIRRQLWLTGAGEGPAPNLFQLLVQIREEEAKEEEEEAEATL 344
                                                    ATLPDKLRDKLKLMKQRRKP-PGFLALVKLLR-----EEEEWEATL 340
                                                                                         GSVESSRDAQIKFLNTYQNPGEKLSAYVIRLEPLLQKVVEKGAIDKDNVNQARLEQVIAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----GED-HGQATYPKAENQTPGREGPQAAGEELGNEAGAGAMSHPK 448
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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297

237

177

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TITLE OF INVENTION MEMBRANE ASSOCIATED PROTEINS
FILE REFERENCE: PF-0731-1 USA
CURRENT APPLICATION NUMBER: US/09/969,680A
CURRENT FILING DATE: 2001-10-02
PRIOR APPLICATION NUMBER: US/09/22315
PRIOR FILING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: 60/149,641
PRIOR FILING DATE: 1999-08-17
PRIOR APPLICATION NUMBER: 60/14,203
PRIOR APPLICATION NUMBER: 60/164,203
PRIOR APPLICATION NUMBER: 60/164,203
PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 74
SOFTWARE: PERL PrOGram
SEQ ID NO 7
                  Sequence 1, Application US/0996529
Publication No. US20020182671A1
GENERAL INFORMATION:
APPLICANT: LAL, Preeti
APPLICANT: TAUG, Y. Tom
APPLICANT: TANG, Y. Tom
APPLICANT: BANDMAN, Olga
APPLICANT: BURFORD, Neil
APPLICANT: BURFORD, Neil
APPLICANT: BURFORD, Neil
APPLICANT: BURGNY, Yalda
APPLICANT: BAUGHN, Mariah R.
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FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte
US-09-969-680A-7
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US-09-969-680A-7
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                                                                                                                                                                                                                                    US-09-965-529-1
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Best Local Simi
Matches 172;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: LAL, Preeti; YUE, Henry APPLICANT: TANG, Y. Tom; BANDMAN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 DAWLEHTTEMLOMWQVPEGEKRRLMECLRGPALQVVSGLRASNASITVEECLAALQQVF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 NRVIGSDINCSAPRVIISPEFWIWAQTIGAAVQPILEQMLYREIRVFSGNIISIPGALAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60 NAKAALLELTGAVDYAAIPREMPGKGGVWKVLFKPPTSDAEFLERLHLFLAREGWTVQDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 NAQAILLELAQDIDYALLPREIPGKGGPWEVIVKPRNSDGEFLNRLNRFLEEERRTVSDM 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MPLTILQDWCRGEHLNTKRCMLILGIPEDCGEDEFEETLQEACRHLGRYRVIGRMFRREE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DPWLEHTNEVLEEWQV6DVEXRRLME6LRGPAADVIRILKSNNPAITTAECLKALEQVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TANG, Y. Tom; BANDMAN, Olga
BURFORD, Neil; AZIMZAI, Yalda
BAUGHN, Mariah R.; LU, Dyung Aina M.
PATTERSON, Chandra
                                                                                                                                                                                                                                                                                                                                                                   ATLPDKLRDKLKLMKQRRKP-PGFLALVKLLR-----EEEEEWEATL 340
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Dyung Aina
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; Pred. No. 3.3e-65;
52; Mismatches 113;
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APPLICANT: Vernet, Corine
APPLICANT: Fernandes, Elma
APPLICANT: Fernandes, Elma
APPLICANT: Shankets, Richard
APPLICANT: Spaderna, Steven
APPLICANT: Spaderna, Steven
APPLICANT: Majunder, Kumud
TITLE OF INVENTION: Movel Polypeptides and Nucleic Acids Encoding Same
FILE REFERENCE: 15966-721 US
CURRENT APPLICATION NUMBER: US/09/804,014A
CURRENT FILING DATE: 2000-03-10
PRIOR APPLICATION NUMBER: 60/188,316
PRIOR APPLICATION NUMBER: 60/188,277
PRIOR APPLICATION NUMBER: 60/189,139
PRIOR FILING DATE: 2000-03-14
PRIOR APPLICATION NUMBER: 60/189,139
PRIOR APPLICATION NUMBER: 60/189,140
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, NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID
US-09-965-529-1
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US-09-804-014A-16
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TITLE OF INVENTION: MEMBRANE ASSOCIATED PROTEINS
FILE REFERENCE: PF-0731 USA
CURRENT APPLICATION NUMBER: US/09/965,529
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 60/149,641; 60/164,203; PCT/US00/22315
PRIOR FILING DATE: 1999-08-17; 1999-11-09; 2000-08-14
NUMBER OF SEQ ID NOS: 74
SOFTWARE: PERL Program
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 16, Application US/09804014A Publication No. US20030064489A1 GENERAL INFORMATION:
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Matches
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TYPE: PRT
ORGANISM: Homo
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APPLICANT: Padig
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Padigaru, Muralidhara
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299 298

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APPLICANT: LAL, Preeti; YUE, Henry
APPLICANT: TANG, Y. Tom; BANDWAN, Olga
APPLICANT: BURFORD, Neil; AZINZAI, Yalda
APPLICANT: BAUGHN, Mariah R.; LU, Dyung Aina M.
APPLICANT: BAUGHN, Mariah R.; LU, Dyung Aina M.
APPLICANT: PATTERSON, Chandra
TITLE OF INVENTION: MEMBRANE ASSOCIATED PROTEINS
FILE REFERENCE: PF-0731-1 USA
CURRENT APPLICATION NUMBER: US/09/969,680A
CURRENT FILING DATE: 2001-10-02
PRIOR APPLICATION NUMBER: US/0/22315
PRIOR APPLICATION NUMBER: 600/22315
PRIOR APPLICATION NUMBER: 60/149,641
PRIOR FILING DATE: 1999-08-17
PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 74
SOFTWARE: PERL PROGRAM
SEQ ID NO 1
LENGTH: 351
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US-09-969-680A-1
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Best Local Similarity 46.6
Matches 165; Conservative
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SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 16
LENGTH: 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/09969680A Publication No. US20030124649A1
Query Match
Best Local Similarity
Matches 165; Conserv
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ORGANISM: Homo sapiens
-09-804-014A-16
                                                                                 NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. US20030124649A1 112301CD1
-09-969-680A-1
                                                                                                                                               ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                                                        TYPE: PRT
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Conservative
                   31.7%;
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46.6%; Pred. No. 1e-60;
vative 60; Mismatches 1
60;
Score 768.5; DB Pred. No. 1e-60; 0; Mismatches 1
                                       DB 10;
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                                       Length 351;
Indels
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11;
  Gaps
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ITITLE OF INVENTION: Differentially Regulated Pro
FILE REFERENCE: 9U 204 205 RI
CURRENT APPLICATION NUMBER: US/10/541,434
CURRENT FILING DATE: 2003-07-18
PRIOR APPLICATION NUMBER: US 60/348,164
PRIOR REILING DATE: 2002-01-15
PRIOR APPLICATION NUMBER: US 60/348,119
PRIOR APPLICATION NUMBER: US 60/348,119
PRIOR APPLICATION NUMBER: US 60/348,119
PRIOR PILING DATE: 2002-01-15
NUMBER OF SEQ ID NOS: 238
SOFTWARE: Patentin version 3.1
SEQ ID NO 10
LENGTH: 351
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(S-10-341-434-10)
; Sequence 10, Application US/10341434
; Publication No. US20030215835A1
; GENERAL INFORMATION:
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Best Local Simi
Matches 165;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              31.7%; Score 768.5; DB Jocal Similarity 46.6%; Pred. No. 1e-60; hes 165; Conservative 60; Mismatches 1
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                                                                                                                           NRVLGSDTNCSAPRVTISPEFWT--WAQTLGAAVQPLLEQMLYRELRVFSGNTISIPGAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MPLTLLQDWCRGEHLNTRRCMLILGIPEDCGEDEFEETLQEACRHLGRYRVIGRMFRREE
                                                                    VFGPVESHKIAQVKLCKAYQEAGEKVSSFVLRLEPLLQRAVENNVVSRRNVNQTRLKRVL 298
                                                                                                                                                                                                                                                                                                                                     NAQAILLELAQDIDYALLPREIPGKGGPWEVIVKPRNSDGEFLNRLNRFLEEERRTVSDM 120
                                                                                                                                                                                                                                                                                                                                                                                                                       MPLTLLQDWCRGEHLNTRRCMLILGIPEDCGEDEFEETLQEACRHLGRYRVIGRMFRREE
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  SGATLPDKLRDKLKLMKQRRKPPGFLALVKLLRE---EEEWEATLGPDRESLEG 349
                                            VFGVTDNPRELQVKYLTTYQKDEEKLSAYVLRLEPLLQKLVQRGAIERDAVNQARLDQVI
                                                                                                                                                                                                                                                                                                NRKVALVGLTAETSHALVPKEIPGKGGIWRVIFKPPDPDNTFLSRLNEFLAGEGMTVGEL
                                                                                                                                                                                                                                                                                                                                                                             MTLRLLEDWCRGMDMNPRKALLIAGISOSCSVAEIEEALQAGLAPLGEYRLLGRMFRRDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGA-VHKTIRRELNL-PEDGPAPGFLQLLVLIKDYEAAEEEEALL---QAILEG
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APPLICANT: HIO, YUKL
APPLICANT: OTSUKA, KAORU
APPLICANT: NAGAI, KENIICHI
APPLICANT: IRIE, RYOTARO
APPLICANT: IRIE, RYOTARO
APPLICANT: YOSHIKAWA, TSUTOMU
APPLICANT: YOSHIKAWA, TSUTOMU
APPLICANT: WAGAHARI, KENII :
APPLICANT: NAGHARI, KENII :
APPLICANT: NUMBER: US/10/094,749
CURRENT APPLICATION UNUMBER: US/10/094,749
CURRENT FILING DATE: 2002-03-12
PRIOR APPLICATION NUMBER: 50/350,435
PRIOR APPLICATION NUMBER: JP 2001-328381
PRIOR APPLICATION NUMBER: JP 2001-328381
PRIOR APPLICATION NUMBER: JP 2001-328381
PRIOR FILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 3381
SOFTWARE: PRETENTIN OF SEQ ID NOS: 3381
SOFTWARE: PRETENTIN VEY: 2.1
SEQ ID NO 1978
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; ORGANISM: Homo sapiens
US-10-094-749-1978
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US-10-094-749-1978
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NATAALVELDREVNYALVEREIPGTGGPWNVVFVPRCSGEBFLGLGRVFHFPEQEGQMVE
                                                                                                                                                                                                                                                       AFDAWLEHTTEMLOMWQ-VPEGEKRRRLMECLRGPALOVVSGLRASNASITVEECLAALQ
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OTSUKI, TETSUJI
WAKAMATSU, AI
                                                                                                                                                                                                                                 SFEVWLDHTTEMLHVWQGVSERERRRLLEGLRGTALQLVHALLAENPARTAQDCLAALA
                                                                                                                                                                                                                                                                                                                                                         DMNRVLGSDTNCSAPRVTISPEFWTWAQTLGAAVQPLLEQMLYRELRVFSGNTISIPGAL
  PRPPARI-TGVGAVP----
                                                                                                     LSGATLPDKLRDKLKLMKQRRKPPGFLALVKLLREEEEWEATLG----PDRESLEGLEVA
                                                                                                                                               QVFGDNESQATIRVKCLTAQQQSGERLSAFVLRLEVLLQKAMEKEALARASADRVRLRQM
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YURI
                                                                LTRAHLTEPLDEALRKLRMAGRSPSFLEMLGLVRESEAWEASLARSVRAQTQEGAGARAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 768.5; DB 15;
Pred. No. 1.2e-60;
2; Mismatches 130;
                      -LPASGNSFDARPSQGYR 384
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CCURRENT FILING DATE: 2001-01-04
PRIOR APPLICATION NUMBER: 09/189,527
PRIOR FILING DATE: 1998-11-10
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 329
TYPE: PRT
ORGANISM: homo sapiens
US-10-037-860-4
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                                                                                                                                                                                     Sequence 40, Application US/09804014A
Publication No. US20030064489A1
GENERAL INFORMATION:
APPLICANT: Li, Li
APPLICANT: Padigaru, Muralidhara
APPLICANT: Vernet, Corine
APPLICANT: Fernandes, Elma
APPLICANT: Fernandes, Elma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION
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Best Local Similarity
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APPLICANT: Josep O. Dalmau
APPLICANT: Myrna R. Rosenfeld
APPLICANT: Shimkets, Richard
APPLICANT: Spaderna, Steven
APPLICANT: Majumder, Kumud
TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoding Same
FILE REFERENCE: 15966-721 US
CURRENT APPLICATION NUMBER: US/09/804,014A
CURRENT FILING DATE: 2002-04-24
PRIOR APPLICATION NUMBER: 60/188,316
PRIOR FILING DATE: 2000-03-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   120 ARVLGFQNPTPTPGPEMPAEMLNY--ILDNVIQPLVESIWYKRLTLFSGKGHPRAWRGNF
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Gaps

59

177

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APPLICANT: Shinkets, Richard.
APPLICANT: Spaderna, Steven
APPLICANT: Majumder, Kumud
TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Enc
FILE REFERENCE: 15966-721 US.
CURRENT APPLICATION NUMBER: US/09/804,014A
CURRENT FILING DATE: 2002-04-24
PRIOR APPLICATION NUMBER: 60/188,316
PRIOR APPLICATION NUMBER: 60/188,316
PRIOR FILING DATE: 2000-03-10
PRIOR FILING DATE: 2000-03-10
PRIOR FILING DATE: 2000-03-10
PRIOR APPLICATION NUMBER: 60/188,277
PRIOR FILING DATE: 2000-03-10
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PRIOR FILLIG DATE: 2000-03-10
PRIOR APPLICATION NUMBER: 60/189,139
PRIOR FILLING DATE: 2000-03-13
PRIOR APPLICATION NUMBER: 60/189,140
PRIOR FILLING DATE: 2000-03-14
PRIOR APPLICATION NUMBER: 60/190,401
PRIOR APPLICATION NUMBER: 60/190,401
PRIOR APPLICATION NUMBER: 60/190,401
PRIOR APPLICATION NUMBER: 60/190,401
PRIOR FILLING DATE: 2000-03-17
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                                                                                                                                                                                                                                                                                                                                                                                        Sequence 39, Application US/09804014A Publication No. US20030064489Ai
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Best Local Similarity
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SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 40
LENGTH: 318
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APPLICANT: Pad
APPLICANT: Ver
APPLICANT: Fer
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Vernet, Corine
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PRIOR APPLICATION NUMBER: 60/189,140
PRIOR FILING DATE: 2000-03-14
PRIOR APPLICATION NUMBER: 60/190,401
PRIOR APPLICATION NUMBER: 60/190,401
PRIOR FILING DATE: 2000-03-17
PRIOR PRIOR DATE: 2000-03-17
PRIOR FILING DATE: 2000-03-17
PRIOR FILING DATE: 2000-03-17
PRIOR FILING DATE: 2000-03-17
NUMBER OF SEQ ID NOS: 75
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Best Local Similarity 47.2%;
Matches 152; Conservative 55
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300 AGA-VHKTIRRELNLPEDGPAP 320
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                                                                                                                                      MILRLLEDWCRGMDMNPRKALLIAGISQSCSVAEIEEALQAGLAPLGEYRLLGRMFRRDE
                              SGATLPDKLRDKLKLMKORRKP 320
                                                                 SRALGHENGSLDPEQGMIPEMWAPMLAQAL-EALQPALQCLKYKKLRVFSGRESPEPGES
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Pred. No. 2.2e-58;
5; Mismatches 111
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US-09-804-014A-73
US-09-804-014A-73
ISEQUENCE 73, Application US/09804014A
Publication No. US20030064489A1
IGENERAL INFORMATION:
APPLICANT: Li, Li
APPLICANT: Li, Li
APPLICANT: Padigaru, Muralidhara
APPLICANT: Padigaru, Muralidhara
APPLICANT: Shimkets, Richard
APPLICANT: Shimkets, Richard
APPLICANT: Spaderna, Steven
APPLICANT: Spaderna, Steven
APPLICANT: Majumder, Kumud
TITLE OF INVENTION: NOVel Polypeptides and Nucleic Acids Encoding Sam
FILE REFERENCE: 15966-721 US
CURRENT APPLICATION NUMBER: US/09/804,014A
CURRENT FILING DATE: 2002-04-24
PRIOR APPLICATION NUMBER: 60/188,316
PRIOR APPLICATION NUMBER: 60/188,316
PRIOR APPLICATION NUMBER: 60/188,277
PRIOR APPLICATION NUMBER: 60/189,139
PRIOR FILING DATE: 2000-03-10
PRIOR APPLICATION NUMBER: 60/189,140
PRIOR APPLICATION NUMBER: 60/189,140
PRIOR APPLICATION NUMBER: 60/190,401
PRIOR FILING DATE: 2000-03-14
PRIOR FILING DATE: 2000-03-17

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APPLICANT: Majunder, Kumud
APPLICANT: Majunder, Kumud
TITLE OF INVENTION: Novel polypeptides and Nucleic Acids Encoding Same
FILE REFERENCE: 15966-721 US
CURRENT APPLICATION NUMBER: US/09/804,014A
CURRENT FILING DATE: 2002-04-24
PRIOR APPLICATION NUMBER: 60/188,316
PRIOR APPLICATION NUMBER: 60/188,316
PRIOR FILING DATE: 2000-03-10
PRIOR APPLICATION NUMBER: 60/189,139
PRIOR APPLICATION NUMBER: 60/189,139
PRIOR APPLICATION NUMBER: 60/189,140
PRIOR APPLICATION NUMBER: 60/189,140
PRIOR APPLICATION NUMBER: 60/189,140
PRIOR APPLICATION NUMBER: 60/190,401
PRIOR APPLICATION NUMBER: 60/190,401
PRIOR FILING DATE: 2000-03-14
PRIOR APPLICATION NUMBER: 60/190,401
PRIOR FILING DATE: 2000-03-17
PRIOR FILING DATE: 2000-03-17
PRIOR PRIOR APPLICATION NUMBER: 60/190,401
PRIOR PRIOR APPLICATION NUMBER: 60/190,231
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US-09-804-014A-74
; Sequence 74, Application US/09804014A
; Publication No. US20030064489A1
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west Local Similarity 48.8%;
Matches 148; Conservation
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APPLICANT: Pad
APPLICANT: Ver
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                                                                                                                      PRIOR FILING DATE: 2000-03-17
NUMBER OF SEQ ID NOS: 75
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 74
Query Match
                                                            ORGANISM: Homo
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Shimkets, Richard
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Pred. No. 2.9e-58;
    Score
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US-10-037-860-11
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APPLICANT: Jerome B. Posner
APPLICANT: Josep O. Dalmau
APPLICANT: Myrna R. Rosenfeld
TITLE OF INVENTION: Ma FAMILY POLYPEPTIDES AND ANTI-MA
TITLE OF INVENTION: ANTIBODIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 11, Application US/10037860 Publication No. US20020123114A1
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Best Local Similarity
Matches 135; Conserv
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SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 09/189,527
PRIOR FILING DATE: 1998-11-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: 2581.1004-004
CURRENT APPLICATION NUMBER: US/10/037,860
CURRENT FILING DATE: 2001-01-04
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TYPE: PRT
ORGANISM: homo sapiens
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                                                                                             EGEKVSAYVLRLETLLRKAVEKRAIPRRIADQVRLEQVMAGATLNQMLWCRLRELKDQGP
                                                                                                                                  AGEKVSSFVLRLEPLLQRAVENNVVSRRNVNQTRLKRVLSGATLPDKLRDKLKLMKQRRK 319
                                                                                                                                                                                                                            EKKRWLAESLRGPALDLMHIVQADNPSISVEECLEAFKQVFGSLESRRTAQVRYLKTYQE
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